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SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Young, Robert

<120> Compounds for Targeting

<130> 43191-256808

<140> US 09/825,012

<141> 2001-04-03

<150> US 60/237,159

<151> 2000-10-02

A35  
<150> GB 0008049.9

<151> 2000-04-03

<160> 101

<170> PatentIn version 3.1

<210> 1

<211> 282

<212> PRT

<213> Homo sapiens

<400> 1

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Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
165 170 175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
180 185 190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
195 200 205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
210 215 220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
225 230 235 240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
245 250 255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
260 265 270

Asp His Tyr Pro Val Glu Val Met Leu Lys

275

280

<210> 2  
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<212> DNA  
<213> Homo sapiens

<400> 2  
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cattctcgtc atctctgagg acatcaccat catctcagga tgagggcat gaagctgctg 180  
ggggcgctgc tggcactggc ggccctactg cagggggccg tgtccctgaa gatcgagcc 240  
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300  
gtgcagatcc tgagccgcta tgacatcgcc ctggccagg aggtcagaga cagccacctg 360  
actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420  
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480  
cctgaccagg tgtctgcgtt ggacagctac tactacgatg atggctgcga gccctgcggg 540  
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gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg 960  
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<210> 3  
<211> 260  
<212> PRT  
<213> Homo sapiens

<400> 3

Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met  
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Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr  
20 25 30

Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val  
35 40 45

Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His  
50 55 60

Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr  
65 70 75 80

Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr  
85 90 95

Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu  
100 105 110

Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe  
115 120 125

Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
130 135 140

Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu  
145 150 155 160

Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val  
165 170 175

Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe  
180 185 190

Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His  
195 200 205

Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala  
210 215 220

Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly  
 225 230 235 240

Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu  
 245 250 255

Val Met Leu Lys  
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<210> 4

<211> 783

<212> DNA

<213> Homo sapiens

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 agagacagcc acctgactgc cgtgggaag ctgctggaca acctaatac ggacgcacca 180  
 gacacctatac actacgttgtt cagttagcca ctgggacgga acagctataa ggagcgctac 240  
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 gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg 660  
 ctccgagggg ccgttggcc cgactcggct cttccctta acttccaggc tgcctatggc 720  
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<210> 5

<211> 161

<212> PRT

210  
 211  
 212  
 213  
 214  
 215

<213> Homo sapiens

<400> 5

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Leu  
1 5 10 15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
20 25 30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
35 40 45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
50 55 60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
65 70 75 80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
85 90 95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
100 105 110

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
115 120 125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
130 135 140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
145 150 155 160

Asp

<210> 6

<211> 858

<212> DNA

<213> Homo sapiens

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atgtccaatg	ccaccctcg	cagctacatt	gtgcagatcc	ttagccgcta	cgacatcgcc	180
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aatcaggacg	caccagacac	ctatca	actgcagatg	agccactggg	acgaaacagc	300
tataaggagc	gctacctgtt	cgtgtacagg	cctgaccagg	tgtctgcgg	ggacagctac	360
tactacgatg	atggctgcga	gccctgcggg	aacgacac	tcaaccgaga	gccagccatt	420
gtcaggttct	tctcccggtt	cacagagg	agggagttt	ccattgttcc	cctgcatgcg	480
gccccgggg	acgcagtagc	cgagatcgac	gctctctatg	acgtctac	ggatgtccaa	540
gagaaatggg	gcttgagga	cgtcatgtt	atgggcact	tcaatgcggg	ctgcagctat	600
gtgagacc	cccagtggc	atccatccgc	ctgtggacaa	gccccac	ccagtggctg	660
atccccgaca	gcgctgacac	cacagctaca	cccacgcact	gtgcctatga	caggatcg	720
gttgcagg	tgctgctcc	agggccgtt	gttccc	cggctttcc	cttaacttc	780
caggctgc	atggcctgag	tgaccaactg	gcccaagcca	tcagtgacca	ctatccagtg	840
gaggtgatgc	tgaagtga					858

<210> 7

<211> 721

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

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acctgttgt	ccagtcagag	ccttttat	atgtcaatc	aaaagatcta	cttggcctgg	180
taccagcaga	agccaggtaa	ggctccaaag	ctgctgatct	actgggc	actcactggaa	240
tctggtgtgc	caagcagatt	cagcgtagc	ggtagcggt	ccgactt	cacccatc	300

agcagcctcc agccagagga catcgccacc tactactgcc agcaatatta tagatatcct	360
cggacgttcg gccaaggac caaggtggaa atcaaacgaa ctgtggctgc accatctgtc	420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg	480
ctgaataact tctatcccag agaggccaaa gtacagtggaa aggtggataa cgcctccaa	540
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc	600
agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa	660
gtcacccatc agggcctgag ctgcggcgtc acaaagagct tcaacagggg agagtgttag	720
a	721

&lt;210&gt; 8

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG-1 light chain

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gtgaccatca cctgtaagtc cagtcagagc cttttatata gtagcaatca aaagatctac	180
ttggccttgtt accagcagaa gccaggttaag gtcacaaagc tgctgatcta ctgggcattcc	240
actaggaaat ctggtggtcc aagcagattc agcggtagcg gtagcggtac cgacttcacc	300
ttcaccatca gcagcctcca gccagaggac atcgccacct actactgcca gcaatattat	360
agatatccctc ggacgttcgg ccaaggacc aaggtggaaa tcaaacgaac tgtggctgca	420
ccatctgtct tcattttccc gccatctgat gagcagttga aatctggAAC tgcctctgtt	480
gtgtgcctgc tgaataactt ctatccaga gaggccaaag tacagtggaa ggtggataac	540
gccctccaat cggtaactc ccaggagagt gtcacagagc aggacagcaa ggacagcacc	600
tacagcctca gcagcacccct gacgctgagc aaagcagact acgagaaaca caaagtctac	660
gcctgcgaag tcacccatca gggcctgagc tcgccccgtca caaagagctt caacaggggaa	720
gagtgttaga	730

<210> 9

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 light chain

<400> 9

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu Tyr Ser Ser Asn Gln Lys Ile Tyr Leu Ala Trp Tyr Gln Gln Lys  
50 55 60

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu  
65 70 75 80

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe  
85 90 95

Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr  
100 105 110

Cys Gln Gln Tyr Tyr Arg Tyr Pro Arg Thr Phe Gly Gln Gly Thr Lys  
115 120 125

Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
130 135 140

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
145 150 155 160

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 10

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG-1 heavy chain

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ggaaagggcc tcgagtggggt cgagagatt ttacctggaa gtaataattc tagataacaat 240  
gagaagttca agggcccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgagggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
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aaggcccatt cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
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tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 660  
aacgtgaatc acaagccccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
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gacaaaactc acacatgccc accgtgcccc gcacctgaac tcctgggggg accgtcagtc 780  
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tgcgtgggg tggacgtgag ccacgaagac cctgagggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct ttttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
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<210> 11

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<220>

<221> CDS

<222> (1)..(15)

<223>

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Asp Lys Thr His Thr	
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<210> 12

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid hinge

<400> 12

Asp Lys Thr His Thr  
1 5

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 13

ccgggtaaag ggagcggcgg gctgaagatc gcagcttca ac

42

<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 14

gagagggaca gaggcccatt tccctcgccg cccgacttct ag

42

<210> 15

<211> 18

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Polypeptide linker

&lt;400&gt; 15

Leu	Ser	Leu	Ser	Pro	Gly	Lys	Gly	Ser	Gly	Gly	Leu	Lys	Ile	Ala	Ala
1				5				10					15		

Phe Asn

&lt;210&gt; 16

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide linker

&lt;400&gt; 16

ccgaaaggga gcggcgggct gaagatcgca gccttcaac

39

&lt;210&gt; 17

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide linker

&lt;400&gt; 17

gagagggaca gaggtttcc ctcgccgcc gacttctag

39

&lt;210&gt; 18

&lt;211&gt; 17

&lt;212&gt; PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 18

Leu Ser Leu Ser Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe  
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Asn

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 19

ccggggagcg gcgggctgaa gatcgcagcc ttcaac

36

<210> 20

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 20

gagagggaca gagggccctc gccgcccac ttctag

36

<210> 21

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 21

Leu Ser Leu Ser Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn  
1 5 10 15

<210> 22

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 22

gcacacctgaag ggagcggcg ggctgaagatc gcagccttca ac 42

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 23

ggtgtggcacgg gtcgtggact tccctcgccg cccgacttct ag 42

<210> 24

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 24

Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala  
1                   5                   10                   15

Phe Asn

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 25

gcacacctgaag gcgggctgaa gatcgcagcc ttcaac

36

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 26

ggtggcacgg gtcgtggact tccgccccgac ttctag

36

<210> 27

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 27

Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn  
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<210> 28

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 28

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<210> 29

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

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<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 30

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
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Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe  
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<210> 31

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 31

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<210> 32

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 32

ctgttttagt tgtgtacgac acagctcaca ggtggcacag gtcgtggct cccg       54

<210> 33

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 33

Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
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Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe
			20			25		

<210> 34

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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tgcaaggcctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tgcagtgggt	cgagagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagtca	agggccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccttgtt	ttgcttactg	gggccaaggg	actctggtca	cagtctcctc	agcctccacc	420
aaggcccatt	cggcttcccc	cctggcaccc	tccccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtaa	ggactacttc	cccgaaaccgg	tgacggtgtc	gtggaaactca	540
ggcgccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600
tccctcagca	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720

gacaaaactc acacatgccc accgtgccc gcacctgaag ggagcggcgg gctgaagatc	780
gcagcattca acatccagac atttggggag accaagatgt ccaatgccac cctcgctcagc	840
tacatttgtc agatcctgag ccgctacgac atcgccctgg tccaggaggt cagagacagc	900
cacctgactg ccgtgggaa gctgctggac aacctcaatc aggacgcacc agacacctat	960
cactacgtgg tcagtgagcc actgggacgg aacagctata aggagcgcta cctgttcgtg	1020
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tgcgggaacg acaccttcaa ccgagagcca gccattgtca gtttcttctc ccggttcaca	1140
gaggtcaggg agttgccat tttccctg catcgcccc cggggacgc agtagccgag	1200
atcgacgctc tctatgacgt ctacctggat gtccaaagaga aatggggctt ggaggacgta	1260
atgttcatgg gcaacttcaa tgcggctgc agctatgtga gaccctccca gtggtcatcc	1320
atccgcctgt ggacaagccc cacctccag tggctgatcc ccgacagcgc tgacaccaca	1380
gctacaccca cgcaactgtgc ctatgacagg atcgtggttt cagggatgct gctccgaggg	1440
gccgttgttc ccgactcggc tttcccttt aacttccagg ctgcctatgg cctgagtgac	1500
caactggccc aagccatcag tgaccactat ccagtggagg tcatgctgaa gtga	1554

<210> 35

<211> 1554

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 35

atgggatgga gctgttatcat ccttttttg gtagcaacag ctacaggtgt ccactccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg ggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataaat	240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccttgtt ttgcctactg gggccaagg actctggtca cagtctcctc agcctccacc	420
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480

gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtgac	gtggaaactca	540
ggcgccctga	ccagcggcgt	gcacaccccttc	ccggctgtcc	tacagtccctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaattttgt	720
gacaaaactc	acacatgtcc	accgtgtcca	gcaccagagg	ggagcggcgg	gctgaagatc	780
gcagccttca	acatccagac	atttggggag	accaagatgt	ccaatgccac	cctcgctcagc	840
tacatttgtc	agatccttag	ccgctacgac	atcgccctgg	tccaggaggt	cagagacagc	900
cacctgactg	ccgtgggaa	gctgctggac	aacctcaatc	aggacgcacc	agacacctat	960
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atcgacgctc	tctatgacgt	ctacctggat	gttcaagaga	aatggggctt	ggaggacgtc	1260
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gctacaccca	cgcactgtgc	ctatgacagg	atcggttttgc	cagggatgct	gctccgaggg	1440
gccgttgttc	ccgactcggc	tcttcccttt	aacttccagg	ctgcctatgg	cctgagtgac	1500
caactggccc	aagccatcag	tgaccactat	ccagtggagg	tgatgctgaa	gtga	1554

<210> 36

<211> 1563

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 36	60					
gccgccacca	tggatggag	ctgtatcatc	ctcttcttgg	tagcaacagc	tacaggtgtc	60
cactcccaagg	tgcagctgg	gcagtctgg	gcagaggtga	aaaaggctgg	ggcctcagtg	120
aagggtgtcct	gcaaggcttc	tggctacacc	ttcagtgct	actggataga	gtgggtgcgc	180

caggctccag gaaaggcct cgagtggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtctatta ctgtgcaaga	360
tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggcac agtctcctca	420
gcctccacca agggcccatac ggtctcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctggtaag gactacttcc ccgaaccggt gacggtgtcg	540
tggaactcag gcgcctgac cagcggcgtg cacaccccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacccagacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaaactca cacatgtcca ccgtgtccag caccagaggg gagcggcggg	780
ctgaagatcg cagccttcaa catccagaca tttggggaga ccaagatgtc caatgccacc	840
ctcgtcagct acattgtgca gatcctgagc cgctacgaca tcgcctgggt ccaggaggc	900
agagacagcc acctgactgc cgtgggaaag ctgctggaca acctcaatca ggacgcacca	960
gacacctatac actacgtggc cagttagcca ctgggacgga acagctataa ggagcgctac	1020
ctgttcgtgt acaggcctga ccaggtgtct gcgggtggaca gctactacta cgatgtatggc	1080
tgcgagccct gcgggaacga caccttcaac cgagagccag ccattgtcag gttcttctcc	1140
cggttcacag aggtcagggc gtttgccatt gttccctgc atgcggccccc gggggacgca	1200
gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg	1260
gaggacgtca tggatggg cgacttcaat gcgggctgca gctatgtgag accctccag	1320
tggtcatcca tccgcctgtg gacaaggcccc accttccagt ggctgatccc cgacagcgct	1380
gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg	1440
ctccgagggg ccgttggcc cgactcggtcttta acttccaggc tgcctatggc	1500
ctgagtgacc aactggccca agccatcagt gaccactatc cagtggaggt gatgctgaag	1560
tga	1563

<210> 37

<211> 1554

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1554)

&lt;223&gt;

<400>	37		
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt			48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag			96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20	25	30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc			144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc			192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat			240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85	90	95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100	105	110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115	120	125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130	135	140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg			528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
165	170	175	

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	576
180 185 190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	624
195 200 205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	672
210 215 220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	720
225 230 235 240	
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggg agc ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly	768
245 250 255	
ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys	816
260 265 270	
atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg	864
275 280 285	
tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala	912
290 295 300	
gtg ggg aag ctg ctg gac aac ctc aat cag gag gca cca gac acc tat Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr	960
305 310 315 320	
cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc tat aag gag cgc His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg	1008
325 330 335	
tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr	1056
340 345 350	
tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg	1104
355 360 365	
gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu	1152
370 375 380	
ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu	1200
385 390 395 400	
atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly	1248
405 410 415	

ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr 420 425 430	1296
gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr 435 440 445	1344
ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr 450 455 460	1392
cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly 465 470 475 480	1440
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr 485 490 495	1488
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val 500 505 510	1536
gag gtg atg ctg aag tga Glu Val Met Leu Lys 515	1554
 <b>&lt;210&gt; 38</b>	
<b>&lt;211&gt; 517</b>	
<b>&lt;212&gt; PRT</b>	
<b>&lt;213&gt; Artificial Sequence</b>	
 <b>&lt;220&gt;</b>	
<b>&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion</b>	
<b>&lt;400&gt; 38</b>	
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15	
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Leu	

50	55	60
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn		
65	70	75
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn		
85	90	95
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100	105	110
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly		
115	120	125
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser		
130	135	140
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala		
145	150	155
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val		
165	170	175
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala		
180	185	190
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val		
195	200	205
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His		
210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225	230	235
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly		
245	250	255
Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys		
260	265	270
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg		
275	280	285

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
 290 295 300

Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr  
 305 310 315 320

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
 325 330 335

Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
 340 345 350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg  
 355 360 365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
 370 375 380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
 385 390 395 400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
 405 410 415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
 420 425 430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
 435 440 445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
 450 455 460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
 465 470 475 480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
 485 490 495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
 500 505 510

Glu Val Met Leu Lys  
 515

<210> 39  
 <211> 1584  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 39	
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gtcagctgg tgcagtctgg ggcagagggtg aaaaagcctg ggcctcagt gaaggtgtcc	120
tgcaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtca gacagcacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctggc ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc	420
aaggcccatt cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gcctggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggactca	540
ggccccctga ccagcggcgt gcacacccctc cccgctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgtcc accgtgtcca gcaccagagg ggagcggcgg gctgaagatc	780
gcagccttca acatccagac atttggggag accaagatgt ccaatgccac cctcgctcagc	840
tacattgtgc agatcctgag ccgctacgac atcggccctgg tccaggaggt cagagacagc	900
cacctgactg ccgtgggaa gctgctggac aacctcaatc aggacgcacc agacacctat	960
cactacgtgg tcagtgagcc actggacgg aacagctata aggacgccta cctgttcgtg	1020
tacaggcctg accaggtgtc tgcgggtggac agctactact acgatgtatgg ctgcgagccc	1080
tgcgggaacg acaccccaa ccgagagcca gccattgtca gtttcttc cccgttcaca	1140
gaggtcaggg agtttgcacat tggcccttg catgcggccc cggggacgc agtagccgag	1200
atcgacgctc tctatgacgt ctacctggat gtccaagaga aatggggctt ggaggacgtc	1260
atgttcatgg gcgacttcaa tgcgggtgc agctatgtga gaccctccca gtggtcatcc	1320

atccgcctgt ggacaagccc cacttccag tggctgatcc ccgacagcgc tgacaccaca	1380
gctacaccca cgcaactgtgc ctatgacagg atcgtggttg cagggatgct gctccgaggg	1440
gccgttgttc ccgactcggc tcttcccttt aacttccagg ctgcctatgg cctgagtgac	1500
caactggccc aagccatcag tgaccactat ccagtggagg tcatgtgaa gggggcgga	1560
ccccaaaaaga agcgcaaggt ttga	1584

<210> 40

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 40	
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gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctggc ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc	420
aaggggccat cggcttcccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggcgt gcctggtaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca	540
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgtcc accgtgtcca gcaccagagg ggagcggcgg gctgaagatc	780
gcagccttca acatccagac atttggggag accaagatgt ccaatgccac cctcgctcagc	840
tacattgtgc agatcctgag ccgctacgac atcgccctgg tccaggaggt cagagacagc	900
cacctgactg ccgtggggaa gctgctggac aacctcaatc aggacgcacc agacacctat	960

cactacgtgg tcagtgagcc actgggacgg aacagctata aggagcgcta cctgttcgtg	1020
tacaggcctg accaggtgtc tgccgtggac agctactact acgatgatgg ctgcgagccc	1080
tgcgggaacg acaccttcaa ccgagagcca gccattgtca gtttcttctc ccggttcaca	1140
gaggtcaggg agttgccat tttccctgt catcgccccc cgggggacgc agtagccgag	1200
atcgacgctc tctatgacgt ctacctggat gtccaagaga aatggggctt ggaggacgtc	1260
atgttgatgg gcgacttcaa tgcgggctgc agctatgtga gaccctccca gtggtcatcc	1320
atccgcctgt ggacaagccc caccccttccag tggctgatcc ccgacagcgc tgacaccaca	1380
gctacaccca cgcaactgtgc ctatgacagg atcgtggttt cagggatgct gctccgaggg	1440
gccgttgttc ccgactcggc tttcccttt aacttccagg ctgcctatgg cctgagtgac	1500
caactggccc aagccatcag tgaccactat ccagtggagg tcatgctgaa ggggggcccc	1560
cccaaaaaga agcgaaggt ttga	1584

<210> 41

<211> 1593

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 41	
gccgccacca tggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc	60
cactcccagg tgcagctggc gcagtctgg gcagaggtga aaaagcctgg ggcctcagtg	120
aagggtgcct gcaaggcttc tggctacacc ttcagtgct actggataga gtgggtgcgc	180
caggctccag gaaaggccct cgagtggcgc ggagagattt tacctggaaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctgggt tgcttactgg gccaaggga ctctggcac agtctcctca	420
gcctccacca agggccatc ggtctcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctggcgtc cttggtaag gactacttcc ccgaaccggc gacgggtgtcg	540
tggaaactcag gcccctgac cagcggcgtc cacaccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacccagacc	660

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aatcttgtc acaaaaactca cacatgtcca ccgtgtccag caccagaggg gagcggcgaa	780
ctgaagatcg cagccttcaa catccagaca ttggggaga ccaagatgtc caatgccacc	840
ctcgtagct acattgtgca gatcctgagc cgctacgaca tcgccttgtt ccaggaggta	900
agagacagcc acctgactgc cgtgggaag ctgctggaca acctaataca ggacgcacca	960
gacacctatac actacgttgtt cagttagcca ctgggacgga acagctataa ggagcgctac	1020
ctgttcgtgt acaggcctga ccaggtgtct gcgggtggaca gctactacta cgatgtatggc	1080
tgcgagccct gcgggaacga cacttcaac cgagagccag ccattgtcag gttttctcc	1140
cggttcacag aggtcaggaa gtttgcatt gttccctgc atgcggcccc gggggacgca	1200
gtagccgaga tcgacgctct ctatgacgtc tacctggatg tccaagagaa atggggcttg	1260
gaggacgtca tgttgatggg cgacttcaat gcgggctgca gctatgtgag accctccag	1320
tggtcatcca tccgcctgtg gacaaggcccc accttccagt ggctgatccc cgacagcgct	1380
gacaccacag ctacacccac gcactgtgcc tatgacagga tcgtgggtgc agggatgctg	1440
ctccgagggg ccgttgttcc cgactcggtcttta acttccaggc tgcctatggc	1500
ctgagtgacc aactggccca agccatcagt gaccactatac cagttggaggt gatgctgaag	1560
gggggcggac ccaaaaagaa gcgcaggatt tga	1593

<210> 42

<211> 1584

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1584)

<223>

<400> 42

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15	48
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggg agc ggc Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly 245 250 255	768
ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys 260 265 270	816
atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg 275 280 285	864
tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala 290 295 300	912
gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr 305 310 315 320	960
cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc tat aag gag cgc His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg 325 330 335	1008
tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr 340 345 350	1056
tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg 355 360 365	1104
gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu 370 375 380	1152
ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu 385 390 395 400	1200
atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly 405 410 415	1248
ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr 420 425 430	1296
gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr 435 440 445	1344
ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr 450 455 460	1392
cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly	1440

465	470	475	480	
gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr 485				1488
490				495
ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val 500				1536
505				510
gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag cgc aag gtt tga Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys Val 515				1584
520				525
<210> 43				
<211> 527				
<212> PRT				
<213> Artificial Sequence				
<220>				
<223> Humanised HMFG1 Fd - DNase I fusion				
<400> 43				
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1                   5                   10                   15				
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20               25                   30				
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35               40                   45				
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50               55                   60				
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65               70                   75                   80				
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85               90                   95				
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100              105                   110				

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Ser Gly  
 245 250 255

Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
 260 265 270

Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg  
 275 280 285

Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala  
 290 295 300

Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr  
 305 310 315 320

His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg  
 325 330 335

Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr  
 340 345 350

Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg  
 355 360 365

Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu  
                  370                   375                   380

Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu  
385 390 395 400

Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly  
405 410 415

Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr  
420 425 430

Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr  
435 440 445

Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr  
450 455 460

His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly  
465 470 475 480

Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr  
485 490 495

Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
500 505 510

Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys Arg Lys Val  
515 520 525

<210> 44

<211> 2196

<212> DNA

### <213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 44	
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtca act agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaaggg actctggtca cagtcctc cgcctccacc	420
aaggcccatt cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacacccctc cccgctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgcccc gcacctgaac tcctgggggg accgtcagtc	780
ttcctcttcc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtccctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctt ccaacaaagc cctccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggtaa gcctgaccc cctggtcaaa ggcttctatc ccagcgacat cggcgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tctcctcta cagcaagctc accgtggaca agagcagggtg gcagcagggg	1320
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccggtaa agggagcggc gggctgaaga tcgcagcctt caacatccag	1440
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agccgctacg acatcgccct ggtccaggag gtcagagaca gccacctgac tgccgtgggg	1560
aagctgctgg acaacctcaa tcaggacgca ccagacaccc atcactacgt ggtcagtgag	1620
ccactgggac ggaacagcta taaggagcgc tacctgttcg tgtacaggcc tgaccagggtg	1680
tctgcggtgg acagctacta ctacgatgtat ggctgcgagc cctgcggaa cgacaccc	1740

aaccgagagc cagccattgt caggttcttc tcccggttca cagaggtcag ggagttgcc	1800
attgttcccc tgcattgcggc cccggggac gcagtagccg agatcgacgc tctctatgac	1860
gtctacctgg atgtccaaga gaaatggggc ttggaggacg tcattgtat gggcgacttc	1920
aatgcgggct gcagctatgt gagaccctcc cagtggcat ccatccgcct gtggacaagc	1980
cccaccttcc agtggctgat cccgcacacg cgtgacacca cagctacacc cacgcactgt	2040
gcctatgaca ggatcgttgt tgcaaggatg ctgctccgag gggccgttgt tcccgactcg	2100
gctctccct ttaacttcca ggctgcctat ggcttgatg accaactggc ccaagccatc	2160
agtgaccact atccagtgga ggtgatgctg aagtga	2196

&lt;210&gt; 45

&lt;211&gt; 2196

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2196)

&lt;223&gt;

&lt;400&gt; 45

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1	5
	10
	15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
20	25
	30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
35	40
	45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc	192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50	55
	60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat	240
---	-----

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85	90	95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100	105	110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115	120	125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130	135	140	
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg			528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
165	170	175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct			576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			
180	185	190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg			624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
195	200	205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac			672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			
210	215	220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt			720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
225	230	235	240
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg			768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly			
245	250	255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg			816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met			
260	265	270	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac			864
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His			
275	280	285	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg			912
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val			
290	295	300	

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg ggt aaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln 465 470 475 480	1440
aca ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile 485 490 495	1488
gtg cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg 500 505 510	1536
gac agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln 515 520 525	1584
gac gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg 530 535 540	1632

aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val 545 550 555 560	1680
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly 565 570 575	1728
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg 580 585 590	1776
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro 595 600 605	1824
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp 610 615 620	1872
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe 625 630 635 640	1920
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg 645 650 655	1968
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp 660 665 670	2016
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala 675 680 685	2064
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe 690 695 700	2112
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile 705 710 715 720	2160
agt gac cac tat cca gtg gag gtg atg ctg aag tga Ser Asp His Tyr Pro Val Glu Val Met Leu Lys 725 730	2196

<210> 46  
<211> 731  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 46

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10				15		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
				20				25				30			

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
				35			40				45				

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				50			55				60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65				70					75				80		

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
				85				90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
				115			120				125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
				130			135				140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150				155			160			

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
				165				170				175			

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				180				185			190				

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				195			200				205				

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
 465 470 475 480

Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
 485 490 495

Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
 500 505 510

Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525

Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
 530 535 540

Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val  
 545 550 555 560

Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly  
 565 570 575

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg  
 580 585 590

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro  
 595 600 605

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp  
 610 615 620

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe  
 625 630 635 640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg  
 645 650 655

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp  
 660 665 670

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala

675

680

685

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe  
690 695 700

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile  
705 710 715 720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys  
725 730

<210> 47

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 47

atggggatgga gctgttatcat cctttcttg gtagcaacag ctacagggtgt ccactccca 60  
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 120  
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaaacac agcctacatg 300  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
tttgcctggt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc 420  
aagggccat cggtcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 480  
gccctgggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca 540  
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac 600  
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc 660  
aacgtgaatc acaagcccaag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
gacaaaactc acacatgccc accgtgcccc gcacctgaac tcctgggggg accgtcagtc 780  
ttcctttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca 840  
tgcgttgtgg tqqacgtqaq ccacqaaqac cctgagggtca agttcaactq qtacqgtqac 900

ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctt ccaacaaagc cctcccgacc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacctg cctggtaaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ctccgaaggg gagcggcggg ctgaagatcg cagcattcaa catccagaca	1440
tttggggaga ccaagatgtc caatgccacc ctcgtcagct acatttgca gatcctgagc	1500
cgctacgaca tcgcccgtt ccaggaggc agagacagcc acctgactgc cgtggggaaag	1560
ctgctggaca acctcaatca ggacgcacca gacacctatc actacgttgt cagtgagcca	1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccaggtgtct	1680
gcgggtggaca gctactacta cgatgatggc tgcgagccct gcgggaacga caccttcaac	1740
cgagagccag ccattgtcag gttttctcc cggttcacag aggtcaggga gtttgccatt	1800
gttccctgc atgcggcccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc	1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tggtatggg cgacttcaat	1920
gcgggctgca gctatgtgag accctccag tggcatcca tccgcctgtg gacaagcccc	1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacacccac gcactgtgcc	2040
tatgacagga tcgtggttgc agggatgctg ctccgagggg ccgttgttcc cgactcggt	2100
cttccctta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcagt	2160
gaccactatc cagtggaggt gatgctgaag tga	2193

<210> 48

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1) .. (2193)

<223>

<400> 48  
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
48

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag  
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30  
96

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc  
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45  
144

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc  
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60  
192

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat  
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80  
240

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac  
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95  
288

aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc  
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110  
336

tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc  
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125  
384

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg  
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140  
432

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg  
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160  
480

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg  
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175  
528

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct  
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190  
576

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg		624	
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
195	200	205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac		672	
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			
210	215	220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt		720	
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
225	230	235	240
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg		768	
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly			
245	250	255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg		816	
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met			
260	265	270	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac		864	
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His			
275	280	285	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg		912	
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val			
290	295	300	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac		960	
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr			
305	310	315	320
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc		1008	
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly			
325	330	335	
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc		1056	
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile			
340	345	350	
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg		1104	
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val			
355	360	365	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc		1152	
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser			
370	375	380	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag		1200	
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu			
385	390	395	400
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc		1248	
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro			
405	410	415	
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg		1296	
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val			

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	435	440	1344
		445	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	450	455	1392
		460	
ccg aag ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr	465	470	1440
		475	480
ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val	485	490	1488
		495	
cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp	500	505	1536
		510	
agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp	515	520	1584
		525	
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn	530	535	1632
		540	
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser	545	550	1680
		555	560
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn	565	570	1728
		575	
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe	580	585	1776
		590	
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly	595	600	1824
		605	
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val	610	615	1872
		620	
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn	625	630	1920
		635	640
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu	645	650	1968
		655	
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc			2016

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr			
660	665	670	
aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg			2064
Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly			
675	680	685	
atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac			2112
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn			
690	695	700	
ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt			2160
Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser			
705	710	715	720
gac cac tat cca gtg gag gtg atg ctg aag tga			2193
Asp His Tyr Pro Val Glu Val Met Leu Lys			
725	730		

&lt;210&gt; 49

&lt;211&gt; 730

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 49

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20	25	30	

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85	90	95	

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350  
  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365  
  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380  
  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400  
  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415  
  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430  
  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445  
  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460  
  
 Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480  
  
 Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495  
  
 Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510  
  
 Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525  
  
 Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540  
  
 Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560  
  
 Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn

565

570

575

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 580 585 590

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 595 600 605

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
 610 615 620

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
 625 630 635 640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
 645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
 660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
 675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
 690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
 705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys  
 725 730

<210> 50

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 50

atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacaggtgt ccactcccg 60

gtgcagctgg tgcaaggctt	120
tgcagtctgg ggcagaggcgaaaggcc	180
ggcaggtacac cttcagtgcc tactggatag	240
tcgagtgggt cgagagatt ttacctggaa	300
gtaataattc tagatacatg	360
gagaagttca agggccgagt gacagtca	420
actagcacat ccacaaacac	480
gagctcagca gcctgaggc tgaggacaca	540
gccgtctatt actgtgcaag atcctacgac	600
tttgcctggt ttgcttactg gggccaaggg	660
actctggtca cagtctcctc agcctccacc	720
aagggccat cggtttccc cctggcaccc	780
tcctccaaga gcacctctgg gggcacagcg	840
gcccctggct gcctggtcaa ggactacttc	900
cccgaaaccgg tgacggtg	960
gtggaaactca ggcgcctga ccagcggcgt	1020
gcacacccctc cccggctgtcc tacagtcctc	1080
aggactctac tccctcagca gcgtggtgac	1140
cgtccctcc accgacttgg gcacccagac	1200
ctacatctgc aacgtgaatc acaagcccag	1260
caacaccaag gtggacaaga aagttgagcc	1320
caaatcttgt gacaaaactc acacatgccc	1380
accgtgccc gcacctgaac tcctgggggg	1440
accgttcc ccccaaaacc caaggacacc	1500
ctcatgatct cccggacccc tgaggtcaca	1560
ttcctcttcc ccccaaaacc caaggacacc	1620
ccacgaagac cctgaggtca agttcaactg	1680
gtacgtggac ggcgtggagg tgcataatgc	1740
caagacaag ccgcgggagg agcagtacaa	1800
cagcacgtac cgtgtggtca gcgtcctcac	
cgtcctgcac caggactggc tgaatggcaa	
ggagtacaag tgcaagggtct ccaacaaagc	
cctcccagcc cccatcgaga aaaccatctc	
caaagccaaa gggcagcccc gagaaccaca	
ggtgtacacc ctgccccat cccggatga	
gctgaccaag aaccaggtca gcctgacctg	
cctggtaaaa ggcttctatc ccagcgacat	
cgccgtggag tggagagaca atgggcagcc	
ggagaacaac tacaagacca cgcctccgt	
gctggactcc gacggctcct cttcctcta	
cagcaagctc accgtggaca agagcaggtg	
gcagcaggaa aaccgtttct catgctccgt	
gatgtcatgag gctctgcaca accactacac	
gcagaagagc ctctccctgt ccccgggag	
cgccgggctg aagatcgacat cttcaacat	
ccagacattt ggggagacca agatgtccaa	
tgccaccctc gtcagctaca ttgtgcagat	
cctgagccgc tacgacatcg ccctggtcca	
ggaggtcaga gacagccacc tgactgccgt	
ggggaaagctg ctggacaacc tcaatcagga	
cgcaccagac acctatcact acgtggtcag	
tgagccactg ggacggaaca gctataagga	
gctacactg ttcgtgtaca ggcctgacca	
ggtgtctgcgt gtggacagct actactacga	
tgatggctgc gagccctgac ggaacgacac	
cttcaaccga gagccagcca ttgtcaggtt	
cttctcccggttcacagagg tcagggagtt	
tgccattgtt	

ccccctgcatt	cggcccccggg	ggacgcagta	gccgagatcg	acgctctcta	tgacgtctac	1860
ctggatgtcc	aagagaaaatg	gggcttggag	gacgtcatgt	tgatgggcga	cttcaatgcg	1920
ggctgcagct	atgtgagacc	ctcccagtgg	tcatccatcc	gcctgtggac	aagccccacc	1980
ttccagtgac	tgatccccga	cagcgtgac	accacagcta	caccacgca	ctgtgcctat	2040
gacaggatcg	tggttgcagg	gatgctgctc	cgagggggcg	ttgttcccga	ctcggcttct	2100
ccctttaact	tccaggctgc	ctatggcctg	agtgaccaac	tggcccaagc	catcagtgac	2160
cactatccaaq	tqqaqqgtqat	qctqaagtqa				2190

<210> 51

<211> 2190

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2190)

<223>

<400> 51

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atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1          5           10          15

```

48

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

96

```

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          35           40           45

```

144

```

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      50           55           60

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192

```

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn
65          70          75          80

```

gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn	288
85 90 95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	336
100 105 110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly	384
115 120 125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser	432
130 135 140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala	480
145 150 155 160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val	528
165 170 175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala	576
180 185 190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val	624
195 200 205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His	672
210 215 220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys	720
225 230 235 240	
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly	768
245 250 255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	816
260 265 270	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His	864
275 280 285	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	912
290 295 300	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	960

305	310	315	320	
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gag tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325	330	335		1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340	345	350		1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355	360	365		1104
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370	375	380		1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385	390	395	400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405	410	415		1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val 420	425	430		1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435	440	445		1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450	455	460		1392
ccg ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 465	470	475	480	1440
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 485	490	495		1488
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 500	505	510		1536
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 515	520	525		1584
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 530	535	540		1632
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg				1680

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala			
545	550	555	560
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac			1728
Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp			
565	570	575	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca			1776
Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr			
580	585	590	
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac			1824
Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp			
595	600	605	
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa			1872
Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln			
610	615	620	
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg			1920
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala			
625	630	635	640
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg			1968
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp			
645	650	655	
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca			2016
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr			
660	665	670	
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg			2064
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met			
675	680	685	
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc			2112
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe			
690	695	700	
cag gct gcc tat ggc ctg agt gaccaa ctg gcc caa gcc atc agt gac			2160
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp			
705	710	715	720
cac tat cca gtg gag gtg atg ctg aag tga			2190
His Tyr Pro Val Glu Val Met Leu Lys			
725			

&lt;210&gt; 52

&lt;211&gt; 729

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 52

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
						20		25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
					35		40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					50		55					60			

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65				70					75				80		

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85			90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100					105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
				115			120				125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
					130		135				140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150				155			160			

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
					165			170				175			

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
					180			185				190			

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
					195			200				205			

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

210	215	220
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys		
225	230	235
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
245	250	255
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met		
260	265	270
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His		
275	280	285
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val		
290	295	300
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr		
305	310	315
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly		
325	330	335
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile		
340	345	350
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val		
355	360	365
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser		
370	375	380
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu		
385	390	395
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro		
405	410	415
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val		
420	425	430
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met		
435	440	445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 465 470 475 480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 485 490 495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 545 550 555 560

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys  
 725

<210> 53

<211> 2226

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<400> 53						
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gtgcagctgg	tgcagtctgg	ggcagagggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtggtt	cggagagatt	ttacctggaa	gtaataattc	tagatacaat	240
gagaagttca	agggccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggtc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccctgg	ttgcttactg	gggccaaggg	actctggtca	cagtctcctc	agcctccacc	420
aaggcccatt	cggctttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgaaaccgg	tgacggtgtc	gtggaactca	540
ggcgccctga	ccagcggcgt	gcacaccttc	ccggctgtcc	tacagtcttc	aggactctac	600
tccctcagca	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatttgt	720
gacaaaactc	acacatgccc	accgtgccca	gcacctgaac	tcctgggggg	accgtcagtc	780
ttcctcttcc	ccccaaaacc	caaggacacc	ctcatgatct	cccgacccc	tgaggtcaca	840
tgcgtggtgg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	900
ggcgtggagg	tgcataatgc	caagacaaag	ccgcgggagg	agcagtacaa	cagcacgtac	960

cgtgtggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	1020
tgcaaggct	ccaacaaagc	cctcccagcc	cccatcgaga	aaaccatctc	caaagccaaa	1080
gggcagcccc	gagaaccaca	ggtgtacacc	ctgccccat	cccgggatga	gctgaccaag	1140
aaccaggta	gcctgacctg	cctggtcaaa	ggcttctatc	ccagcgacat	cgccgtggag	1200
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctccgt	gctggactcc	1260
gacggctcct	tcttcctcta	cagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1320
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1380
ctctccctgt	ctccggtaa	agggagcggc	gggctgaaga	tcgcagcctt	caacatccag	1440
acatttgggg	agaccaagat	gtccaatgcc	acectcgta	gctacattgt	gcagatcctg	1500
agccgctacg	acatcgccct	ggtccaggag	gtcagagaca	gccacctgac	tgccgtgggg	1560
aagctgctgg	acaaccta	tcaggacgca	ccagacacct	atcaactacgt	ggtcagtgag	1620
ccactgggac	ggaacagcta	taaggagcgc	tacctgttcg	tgtacaggcc	tgaccaggtg	1680
tctgcggtgg	acagctacta	ctacgatgat	ggctgcgagc	cctgcgggaa	cgacaccc	1740
aaccgagagc	cagccattgt	caggttcttc	tcccggttca	cagaggtcag	ggagttgcc	1800
attgttcccc	tgcattgcggc	cccggggac	gcagtagccg	agatcgacgc	tctctatgac	1860
gtctacctgg	atgtccaaga	gaaatggggc	ttggaggacg	tcatgttgat	gggcgacttc	1920
aatgcgggct	gcagctatgt	gagaccctcc	cagtggtcat	ccatccgcct	gtggacaagc	1980
cccaccc	agtggctgat	ccccgacagc	gctgacacca	cagctacacc	cacgcactgt	2040
gcctatgaca	ggatcgttgt	tgcaggatg	ctgctccgag	ggccgttgt	tcccgactcg	2100
gctttccct	ttaacttcca	ggctgcctat	ggcctgagtg	accaactggc	ccaagccatc	2160
agtgaccact	atccagtgga	ggtgatgctg	aagggggggcg	gaccaaaaaa	gaagcgcaag	2220
gtttga						2226

&lt;210&gt; 54

&lt;211&gt; 2226

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2226)

<223>

<400>	54		48
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt			
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag			96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20	25	30	
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc			144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc			192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat			240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85	90	95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100	105	110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115	120	125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130	135	140	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg			528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
165	170	175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct			576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			
180	185	190	

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245 250 255	768
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260 265 270	816
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	1296

420	425	430	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	435	440	1344
		445	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	450	455	1392
		460	
ccg ggt aaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln	465	470	1440
		475	480
aca ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile	485	490	1488
		495	
gtg cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg	500	505	1536
		510	
gac agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln	515	520	1584
		525	
gac gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg	530	535	1632
		540	
aac agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val	545	550	1680
		555	560
tct gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly	565	570	1728
		575	
aac gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Ser Arg	580	585	1776
		590	
ttc aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro	595	600	1824
		605	
ggg gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp	610	615	1872
		620	
gtc caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe	625	630	1920
		635	640
aat gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg	645	650	1968
		655	
ctg tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac			2016

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp			
660	665	670	
acc aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca			2064
Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala			
675	680	685	
ggg atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt			2112
Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe			
690	695	700	
aac ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc			2160
Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile			
705	710	715	720
agt gac cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa			2208
Ser Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys			
725	730	735	
aag aag cgc aag gtt tga			2226
Lys Lys Arg Lys Val			
740			

&lt;210&gt; 55

&lt;211&gt; 741

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 55

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20	25	30	

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85                    90                    95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100                    105                    110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115                    120                    125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130                    135                    140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145                    150                    155                    160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165                    170                    175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180                    185                    190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195                    200                    205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210                    215                    220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225                    230                    235                    240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245                    250                    255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260                    265                    270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275                    280                    285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290                    295                    300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305                    310                    315                    320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
           340                   345                   350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
           355           360           365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370                    375                    380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Pro Gly Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln  
465 470 475 480

Thr Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile  
485 490 495

Val Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg  
500 505 510

Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln  
 515 520 525

Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg  
530 535 540

Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val

545

550

555

560

Ser Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly  
 565 570 575

Asn Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg  
 580 585 590

Phe Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro  
 595 600 605

Gly Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp  
 610 615 620

Val Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe  
 625 630 635 640

Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg  
 645 650 655

Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp  
 660 665 670

Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala  
 675 680 685

Gly Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe  
 690 695 700

Asn Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile  
 705 710 715 720

Ser Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys  
 725 730 735

Lys Lys Arg Lys Val  
 740

<210> 56

<211> 2223

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 56

atgggatgga	gctgttatcat	cctttcttg	gtagcaacag	ctacaggtgt	ccactccag	60
gtgcagctgg	tgcagtctgg	ggcagagggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagttca	aggcccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccttgt	ttgcttactg	gggccaaggg	actctggtca	cagtctcctc	agcctccacc	420
aagggccat	cggcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgaaaccgg	tgacggtg	gtggactca	540
ggcgcctga	ccagcggcgt	gcacacettc	ccggctgtcc	tacagtctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgccc	accgtgcca	gcacctgaac	tcctgggggg	accgtcagtc	780
ttcctttcc	ccccaaaacc	caaggacacc	ctcatgatct	ccggacccc	tgaggtcaca	840
tgcgtggtgg	tggacgtgag	ccacgaagac	cctgaggtca	agttcaactg	gtacgtggac	900
ggcgtggagg	tgcataatgc	caagacaaag	ccgcgggagg	agcagtacaa	cagcacgtac	960
cgtgtggtca	gcgtcctcac	cgtcctgcac	caggactggc	tgaatggcaa	ggagtacaag	1020
tgcaaggct	ccaacaaagc	cctcccagcc	cccatcgaga	aaaccatctc	caaagccaaa	1080
ggcagcccc	gagaaccaca	ggtgtacacc	ctgccccat	cccggtatga	gctgaccaag	1140
aaccaggta	gcctgacctg	cctggtcaaa	ggttctatc	ccagcgacat	cgccgtggag	1200
tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgcctccgt	gctggactcc	1260
gacggctcct	tcttcctcta	cagcaagctc	accgtggaca	agagcaggtg	gcagcagggg	1320
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	1380
ctctccctgt	ctccgaaggg	gagcggcggg	ctgaagatcg	cagcctcaa	catccagaca	1440
tttggggaga	ccaagatgtc	caatgccacc	ctcgtagct	acatttgca	gatcctgagc	1500
cgctacgaca	tcgcccgt	ccaggaggc	agagacagcc	acctgactgc	cgtggggaaag	1560

ctgctggaca acctcaatca ggacgcacca gacaccatac actacgttgt cagtgagcca	1620
ctgggacgga acagctataa ggagcgctac ctgttcgtgt acaggcctga ccaggtgtct	1680
gcggtgtggaca gctactacta cgatgtatggc tgcgagccct gcgggaacga caccttcaac	1740
cgagagccag ccattgtcag gttcttctcc cggttcacag aggtcaggga gtttgccatt	1800
gttccccctgc atgcggccccc gggggacgca gtagccgaga tcgacgctct ctatgacgtc	1860
tacctggatg tccaagagaa atggggcttg gaggacgtca tggtgatggg cgacttcaat	1920
gcgggctgca gctatgtgag accctccca ggtcatcca tccgcctgtg gacaagcccc	1980
accttccagt ggctgatccc cgacagcgct gacaccacag ctacacccac gcactgtgcc	2040
tatgacagga tcgtggttgc agggatgctg ctccgagggg ccgttgttcc cgactcgct	2100
cttccctta acttccaggc tgcctatggc ctgagtgacc aactggccca agccatcaagt	2160
gaccactatac cagtgaggt gatgctgaag gggggcggac ccaaaaagaa gcgcaaggtt	2220
tga	2223

<210> 57

<211> 2223

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

<220>

<221> CDS

<222> (1)..(2223)

<223>

<400> 57

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48		
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly			
1	5	10	15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag	96	
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys		
20	25	30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc	144
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Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35	40	45	
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc			192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50	55	60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat			240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65	70	75	80
gag aag ttc aag ggc cga gtc aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85	90	95	
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100	105	110	
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115	120	125	
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130	135	140	
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			
145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg			528
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val			
165	170	175	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct			576
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala			
180	185	190	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg			624
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val			
195	200	205	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac			672
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His			
210	215	220	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt			720
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys			
225	230	235	240
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg			768
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly			
245	250	255	
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg			816
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met			
260	265	270	

atc tcc cg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275 280 285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290 295 300	912
cat aat gcc aag aca aag ccg cg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr 305 310 315 320	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325 330 335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340 345 350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355 360 365	1104
tac acc ctg ccc cca tcc cg gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg aag ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr 465 470 475 480	1440
ttt ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val 485 490 495	1488
cag atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp 500 505 510	1536

agc cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp 515 520 525	1584
gca cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn 530 535 540	1632
agc tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser 545 550 555 560	1680
gcg gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn 565 570 575	1728
gac acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Ser Arg Phe 580 585 590	1776
aca gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly 595 600 605	1824
gac gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val 610 615 620	1872
caa gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn 625 630 635 640	1920
gcg ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu 645 650 655	1968
tgg aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr 660 665 670	2016
aca gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly 675 680 685	2064
atg ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn 690 695 700	2112
ttc cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser 705 710 715 720	2160
gac cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys 725 730 735	2208
aag cgc aag gtt tga Lys Arg Lys Val	2223

740

&lt;210&gt; 58

&lt;211&gt; 740

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 heavy chain - DNase I fusion

&lt;400&gt; 58

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10				15		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
				20				25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
				35			40				45				

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
				50			55			60					

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
65				70					75			80			

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85			90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
			100				105				110				

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
				115			120				125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
				130			135			140					

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
145					150				155			160			

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460

Pro Lys Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr  
 465 470 475 480

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val  
 485 490 495

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp  
 500 505 510

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp  
 515 520 525

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn  
 530 535 540

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser  
 545 550 555 560

Ala Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
 565 570 575

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe  
 580 585 590

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly  
 595 600 605

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val  
 610 615 620

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn  
 625 630 635 640

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu  
645 650 655

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr  
660 665 670

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
675 680 685

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn  
690 695 700

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser  
705 710 715 720

Asp His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys  
725 730 735

Lys Arg Lys Val  
740

<210> 59

<211> 2220

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 heavy chain - DNase I fusion

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<400> 59
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gtgcagctgg tgcaagtctgg ggcagaggtaaaaaagcctgggcctcagt gaaggtgtcc 120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat 240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300
gagctcagca gcctgaggta tgaggacaca gccgtctatt actgtgcaag atcctacac 360
tttgcctgggtt tgcttactggggactctggta cagtcctcctc agcctccacc 420
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aagggccat cggtttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gcctggct gcctggtaa ggactacttc cccgaaccgg tgacggtgac gtggaaactca	540
ggcgccctga ccagcggcgt gcacacccctc ccggctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacctgaac tcctgggggg accgtcagtc	780
ttcctttcc cccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	840
tgcgtggtgg tggacgtgag ccacgaagac cctgaggtca agttcaactg gtacgtggac	900
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	960
cgtgtggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1020
tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1080
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccggatga gctgaccaag	1140
aaccaggta gcctgacctg cctggtaaaa ggcttctatc ccagcgacat cgccgtggag	1200
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc	1260
gacggctcct tcttcctcta cagcaagctc accgtggaca agagcaggtg gcagcagggg	1320
aacgtttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc	1380
ctctccctgt ccccgggag cggcgggctg aagatcgac cttcaacat ccagacattt	1440
ggggagacca agatgtccaa tgccaccctc gtcagctaca ttgtcagat cctgagccgc	1500
tacgacatcg ccctggtcca ggaggtcaga gacagccacc tgactgccgt ggggaagctg	1560
ctggacaacc tcaatcagga cgcaccagac acctatcact acgtggtcag tgagccactg	1620
ggacggaaca gctataagga gcgctacctg ttcgtgtaca ggcctgacca ggtgtctg	1680
gtggacagct actactacga ttagtggctgc gagccctgac ggaacgacac cttcaaccga	1740
gagccagcca ttgtcaggtt cttctccgg ttcacagagg tcagggagtt tgccattgtt	1800
ccctgcatg cggccccggg ggacgcagta gccgagatcg acgctctcta tgacgtctac	1860
ctggatgtcc aagagaaatg gggcttggag gacgtcatgt ttagtggcga cttcaatgcg	1920
ggctgcagct atgtgagacc ctcccagtgg tcatccatcc gcctgtggac aagccccacc	1980
ttccagtgcc ttagtccccga cagcgctgac accacagcta cacccacgca ctgtgcctat	2040
gacaggatcg tgggtgcagg gatgctgctc cgagggcccg ttgttccga ctggctctt	2100
cccttaact tccaggctgc ctatggctg agtgcaccaac tggcccaagc catcagtgac	2160
cactatccag tggaggtgat gctgaagggg ggcggaccca aaaagaagcg caaggtttga	2220

<210> 60  
<211> 2220  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 heavy chain - DNase I fusion  
<220>  
<221> CDS  
<222> (1)..(220)  
<223>

<400> 60		
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt		48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly		
1                       5                       10                       15		
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag		96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys		
20                     25                       30		
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc		144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
35                     40                       45		
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc		192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
50                     55                       60		
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat		240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn		
65                     70                       75                       80		
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac		288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn		
85                     90                       95		
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc		336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100                   105                       110		
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc		384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly		
115                   120                       125		

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130	135	140	432
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145	150	155	160
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165	170	175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180	185	190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195	200	205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210	215	220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225	230	235	720
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly 245	250	255	768
gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 260	265	270	816
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His 275	280	285	864
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 290	295	300	912
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr 305	310	315	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly 325	330	335	1008
aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile 340	345	350	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val 355	360	365	1104

tac acc ctg ccc cca tcc cg <sup>g</sup> gat gag ctg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser 370 375 380	1152
ctg acc tgc ctg gtc aaa gg <sup>c</sup> ttc tat ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu 385 390 395 400	1200
tgg gag agc aat gg <sup>g</sup> cag cc <sup>g</sup> gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro 405 410 415	1248
gtg ctg gac tcc gac gg <sup>c</sup> tcc ttc ttc ctc tac agc aag ctc acc gtg Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val 420 425 430	1296
gac aag agc agg tgg cag cag gg <sup>g</sup> aac gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met 435 440 445	1344
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser 450 455 460	1392
ccg ggg agc gg <sup>c</sup> ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 465 470 475 480	1440
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 485 490 495	1488
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 500 505 510	1536
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 515 520 525	1584
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 530 535 540	1632
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gc <sup>g</sup> Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala 545 550 555 560	1680
gtg gac agc tac tac tac gat gat gg <sup>c</sup> tgc gag ccc tgc gg <sup>g</sup> aac gac Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp 565 570 575	1728
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 580 585 590	1776
gag gtc agg gag ttt gcc att gtt ccc ctg cat gc <sup>g</sup> gcc cc <sup>g</sup> gg <sup>g</sup> gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp	1824

595	600	605	
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln 610	615	620	1872
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala 625	630	635	1920
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp 645	650	655	1968
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr 660	665	670	2016
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met 675	680	685	2064
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe 690	695	700	2112
cag gct gcc tat ggc ctg agt gaccaa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp 705	710	715	2160
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys 725	730	735	2208
cgc aag gtt tga Arg Lys Val			2220

<210> 61  
<211> 739  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 heavy chain - DNase I fusion  
<400> 61

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 275 280 285

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
305					310					315					320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Pro Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
465 470 475 480

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
485 490 495

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 500 505 510

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 515 520 525

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 530 535 540

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 545 550 555 560

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 565 570 575

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 580 585 590

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 595 600 605

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 610 615 620

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 625 630 635 640

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 645 650 655

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 660 665 670

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
 675 680 685

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
 690 695 700

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
 705 710 715 720

His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys

725

730

735

Arg Lys Val

&lt;210&gt; 62

&lt;211&gt; 1548

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 62

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gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagttca	agggccgagt	gacagtcaet	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgcctgg	ttgcttactg	gggccaagg	actctggtca	cagtctcctc	agcctccacc	420
aaggcccatt	cggcttccc	cctggcaccc	tcctccaaga	gcacctctgg	ggcacacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgaaaccgg	tgacggtg	gtggactca	540
ggcgccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600
tccctcagca	gcgtggtgac	cgtcccc	agcagcttgg	gcaccc	ctacatctgc	660
aacgtgaatc	acaagccc	caacacca	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgccc	accgtgccc	gcacctgaag	gcgggctgaa	gatgcagcc	780
ttcaacatcc	agacatttgg	ggagacca	atgtccaatg	ccaccctcg	cagctacatt	840
gtgcagatcc	tgagccgcta	cgacatcgcc	ctggccagg	aggtcagaga	cagccac	900
actgccgtgg	ggaagctgct	ggacaac	aatcaggac	caccagac	ctatcactac	960
gtggtcagtg	agccactgg	acgaaac	tataagg	gctac	ctgtacagg	1020
cctgaccagg	tgtctcggt	ggacag	tac	atggctgcg	gccctgcgg	1080
aacgacac	tcaaccgaga	gccagccatt	gtcaggttct	tctcccggtt	cacagagg	1140

agggagtttgcattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 1200  
 gctctctatg acgtctacctt gnatgtccaa gagaaatggg gcttggagga cgtcatgtt 1260  
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 1320  
 ctgtggacaa gccccacattt ccagtggctg atccccgaca gcgctgacac cacagctaca 1380  
 cccacgcact gtgccttatga caggatcggt gttgcaggga tgctgctccg aggggccgtt 1440  
 gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg 1500  
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtga 1548

<210> 63

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 63  
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 tgcaaggctt ctggctacac cttagtgcc tactggatag agtgggtgcg ccaggctcca 180  
 ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat 240  
 gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg 300  
 gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
 tttgcctggg ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc 420  
 aagggccat cggctttccc cctggcaccc tcctccaaga gcacccctgg gggcacagcg 480  
 gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgtc gtggaaactca 540  
 ggcgcctgta ccagcggcgt gcacaccccttc ccggctgtcc tacagtccctc aggactctac 600  
 tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc 660  
 aacgtgaatc acaagccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 720  
 gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatgcagcc 780  
 ttcaacatcc agacatttgg ggagaccaag atgtccatg ccaccctcgat cagctacatt 840

gtgcagatcc tgagccgcta cgacatcgcc ctggtccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcaactac	960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc	1140
agggagtttgcattgttcc cctgcatgct gcgggggggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggg cgtcatgttgc	1260
atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggc atccatccgc	1320
ctgtggacaa gccccacctt ccagtggtcg atccccgaca gcgctgacac cacagctaca	1380
cccacgcact gtgccttatga caggatcgat gttgcaggga tgctgctccg agggggccgtt	1440
gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg	1500
qcccaaqcca tcagtqacca ctatccaqtg qaqqtqatqc tqaqgtqa	1548

<210> 64

<211> 1557

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 64

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aagggtgcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc 180  
caggctccag gaaaggcct cgagtggc ggagagattt tacctggaag taataattct 240  
agataacaatg agaagttcaa ggcccgagtg acagtcacta gagacacatc cacaacaca 300  
gcctacatgg agtcagcag cctgaggctt gaggacacag ccgtctatta ctgtgcaaga 360  
tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggcac agtctcccta 420  
gcctccacca agggccatc ggtctcccc ctggcacccct cctccaagag cacctctggg 480  
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccgggt gacgggtgtcg 540  
tqqaactcaq qcqcctqac caqccqgqtc cacacccatc cggctgtcct acqgtcccta 600

ggactctact	ccctcagcag	cgtggtgacc	gtgcctcca	gcagcttggg	cacccagacc	660
tacatctgca	acgtgaatca	caagcccagc	aacaccaagg	tggacaagaa	agttgagccc	720
aatcttgtg	acaaaactca	cacatgtcca	ccgtgtccag	caccagaggg	cgggctgaag	780
atcgcagcct	tcaacatcca	gacatttggg	gagaccaaga	tgtccaatgc	caccctcgtc	840
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acagaggtca	gggagttgc	cattgttccc	ctgcatgcgg	ccccggggga	cgcagtagcc	1200
gagatcgacg	ctctctatga	cgtctacctt	gatgtccaag	agaaatgggg	cttggaggac	1260
gtcatgttga	tggcgactt	caatgcgggc	tgcagctatg	tgagaccctc	ccagtggta	1320
tccatccgcc	tgtggacaag	ccccacattt	cagtggctga	tcccccacag	cgctgacacc	1380
acagctacac	ccacgcactg	tgcctatgac	aggatcgtgg	ttgcaggat	gctgctccga	1440
ggggccgttg	ttcccgactc	ggctcttccc	ttaacttcc	aggctgccta	tggcctgagt	1500
gaccaactgg	cccaagccat	cagtgaccac	tatccagtgg	aggtgatgct	gaagtga	1557

<210> 65

<211> 1548

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1548)

<223>

<400> 65

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gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag· Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu 245 250 255	768
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser 260 265 270	816
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp 275 280 285	864
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly 290 295 300	912
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr 305 310 315 320	960
gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc tat aag gag cgc tac ctg Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu 325 330 335	1008
ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac tac tac Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr 340 345 350	1056
gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga gag cca Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro 355 360 365	1104
gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag ttt gcc Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala 370 375 380	1152
att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag atc gac Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp 385 390 395 400	1200
gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc ttg gag Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu 405 410 415	1248
gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat gtg aga Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg 420 425 430	1296
ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc ttc cag Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln 435 440 445	1344
tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg cac tgt Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys 450 455 460	1392
gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg gcc gtt Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val	1440

465	470	475	480	
gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat ggc ctg Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu 485 490 495				1488
agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg gag gtg Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val 500 505 510				1536
atg ctg aag tga Met Leu Lys 515				1548
 <b>&lt;210&gt; 66</b>				
<b>&lt;211&gt; 515</b>				
<b>&lt;212&gt; PRT</b>				
<b>&lt;213&gt; Artificial Sequence</b>				
 <b>&lt;220&gt;</b>				
<b>&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion</b>				
<b>&lt;400&gt; 66</b>				
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15				
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30				
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45				
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60				
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80				
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95				
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110				

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115                    120                    125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130                    135                    140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145                    150                    155                    160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165                    170                    175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180                    185                    190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195                    200                    205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210                    215                    220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225                    230                    235                    240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Leu  
 245                    250                    255

Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser  
 260                    265                    270

Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp  
 275                    280                    285

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly  
 290                    295                    300

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr  
 305                    310                    315                    320

Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu  
 325                    330                    335

Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr  
 340                    345                    350

Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro  
 355 360 365

Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala  
 370 375 380

Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp  
 385 390 395 400

Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu  
 405 410 415

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
 500 505 510

Met Leu Lys  
 515

<210> 67

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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tgcaaggcct	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180
ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagttca	aggccgagt	gacagtca	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgcctgg	ttgcttactg	gggccaagg	actctggtca	cagtctcctc	agcctccacc	420
aaggcccatt	cggcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgAACGG	tgacgggtgc	gtggaaactca	540
ggcgcctg	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600
tccctcagca	gcgtggtgac	cgtccctc	agcagcttg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatttgt	720
gacaaaactc	acacatgctg	tgtggagtgc	ccaccgtgc	cagcacctga	agggagcggc	780
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accctcgta	gctacattgt	gcagatcctg	agccgctacg	acatcgccct	ggtccaggag	900
gtcagagaca	gccacctgac	tgccgtgggg	aagctgctgg	acaaccta	tcaggacgca	960
ccagacacct	atca	actacgt	ggtcagtgc	ccactggac	gaaacagcta	1020
tacctgttcg	tgtacaggcc	tgaccaggtg	tctgcgg	acagctacta	ctacgatgat	1080
ggctgcgagc	cctgcggaa	cgacaccc	aaccgagac	cagccattgt	caggttctc	1140
tcccggttca	cagaggtcag	ggagttgcc	attgttcccc	tgcatgcggc	cccggggac	1200
gcagtagccg	agatcgacgc	tctctatgac	gtctacctgg	atgtccaaga	gaaatggggc	1260
ttggaggacg	tcatgttgat	ggcgacttc	aatgcgggct	gcagctatgt	gagaccctcc	1320
cagtggtcat	ccatccgcct	gtggacaagc	cccaccc	agtggctgat	ccccgacacg	1380
gctgacacca	cagctacacc	cacgcactgt	gcctatgaca	ggatcgtgg	tgcagggatg	1440
ctgctccgag	ggccgttgt	tcccgactcg	gcttccct	ttaacttcca	ggctgcctat	1500
ggcctgagtg	accaactggc	ccaagccatc	agtgaccact	atccagtgg	ggtgatgctg	1560
aagtga						1566

<211> 1566

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggetcca	180	
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa gtaataattc tagataacaat	240	
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360	
tttgccttgtt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc	420	
aaggggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480	
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggaaactca	540	
ggcgccctga ccagcggcgt gcacacccctc cccgctgtcc tacagtccctc aggactctac	600	
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660	
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gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga ggggagcggc	780	
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tacctgttcg tgtacaggcc tgaccaggtg tctgcgggtgg acagctacta ctacgatgt	1080	
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gcagtagccg agatcgacgc tctctatgac gtctacctgg atgtccaaga gaaatggggc	1260	
ttggaggacg tcatgttgat gggcgacttc aatgcgggct gcagctatgt gagaccctcc	1320	
cagtggtcat ccatccgcct gtggacaagc cccaccttcc agtggctgtat ccccgacagc	1380	

gctgacacca cagctacacc cacgcactgt gcctatgaca ggatcgtgg tgcagggatg	1440
ctgctccgag gggccgttgt tcccgactcg gctttccct ttaacttcca ggctgcctat	1500
ggcctgagtg accaactggc ccaagccatc agtgaccact atccagtgga ggtgatgctg	1560
aagtga	1566

<210> 69

<211> 1575

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 69	
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cactcccagg tgcagctgg gcagtctgg gcagaggtga aaaagcctgg ggcctcagtg	120
aagggtgtcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctggtcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggc gacgggtgtcg	540
tggaaactcag gcgcctgac cagcggcgtg cacaccccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgccttcca gcagcttggg cacccagacc	660
tacatctgca acgtaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaaactca cacatgtgt gtcgagtgatc caccgtgtcc agcaccagag	780
gggagcggcg ggctgaagat cgcagcattc aacatccaga catttgggg gaccaagatg	840
tccaatgcca ccctcgtag ctacattgtg cagatcctga gccgctacga catcgccctg	900
gtccaggagg tcagagacag ccacccgtact gccgtgggg agctgctgga caacctcaat	960
caggacgcac cagacaccta tcaactacgtg gtcagtgagc cactggacg gaacagctat	1020
aaggagcgct acctgttcgt gtacaggcct gaccaggtgt ctgcggtgga cagctactac	1080

## 100

tacgatgatg	gctgcgagcc	ctgcggaaac	gacacattca	accgagagcc	agccattgtc	1140
aggttcttct	cccggttcac	agaggtcagg	gagttgccca	ttgttcccct	gcatgcggcc	1200
ccgggggacg	cagtagccga	gatcgacgct	ctctatgacg	tctacctgga	tgtccaagag	1260
aatggggct	tggaggacgt	catgttgatg	ggcgacttca	atgcggctg	cagctatgtg	1320
agaccctccc	agtggtcata	catccgcctg	tggacaagcc	ccaccccttca	gtggctgatc	1380
cccgacagcg	ctgacaccac	agctacacccc	acgcactgtg	cctatgacag	gatcgtggtt	1440
gcagggatgc	tgctccgagg	ggccgttgtt	cccgactcgg	ctcttccctt	taacttccag	1500
gctgcctatg	gcctgagtga	ccaaactggcc	caagccatca	gtgaccacta	tccagtggag	1560
gtgatgctga	agtga					1575

&lt;210&gt; 70

&lt;211&gt; 1566

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1566)

&lt;223&gt;

&lt;400&gt; 70

atg	gga	tgg	agc	tgt	atc	atc	ctc	ttc	ttg	gta	gca	aca	gct	aca	gg	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1					5				10					15		

gtc	cac	tcc	cag	gtg	cag	ctg	gtg	cag	tct	ggg	gca	gag	gtg	aaa	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
							20		25				30			

cct	ggg	gcc	tca	gtg	aag	gtg	tcc	tgc	aag	gct	tct	ggc	tac	acc	ttc	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
					35				40			45				

agt	gcc	tac	tgg	ata	gag	tgg	gtg	cgc	cag	gct	cca	gga	aag	ggc	ctc	192
Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	

50	55	60	
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80			240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95			288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110			336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125			384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140			432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160			480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175			528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190			576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205			624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220			672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240			720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255			768
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 260 265 270			816
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 275 280 285			864
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc			912

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser			
290	295	300	
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca			960
His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala			
305	310	315	320
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg aac agc			1008
Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser			
325	330	335	
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg			1056
Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala			
340	345	350	
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac			1104
Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp			
355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca			1152
Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr			
370	375	380	
gag gtc agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac			1200
Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp			
385	390	395	400
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa			1248
Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln			
405	410	415	
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg			1296
Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala			
420	425	430	
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg			1344
Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp			
435	440	445	
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca			1392
Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr			
450	455	460	
gct aca ccc acg cac tgt gcc tat gac agg atc gtc gtt gca ggg atg			1440
Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met			
465	470	475	480
ctg ctc cga ggg gcc gtt ccc gac tcg gct ctt ccc ttt aac ttc			1488
Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe			
485	490	495	
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac			1536
Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp			
500	505	510	
cac tat cca gtg gag gtg atg ctg aag tga			1566
His Tyr Pro Val Glu Val Met Leu Lys			
515	520		

&lt;210&gt; 71

&lt;211&gt; 521

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 71

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10				15		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
						20		25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
						35		40				45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					50		55				60				

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
					65		70					75			80

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85			90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
						100		105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
						115		120			125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
						130		135			140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
						145		150			155			160	

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
						165		170				175			

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260 265 270

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275 280 285

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290 295 300

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305 310 315 320

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325 330 335

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340 345 350

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355 360 365

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370 375 380

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385 390 395 400

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln

105

405

410

415

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
420 425 430

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
435 440 445

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
450 455 460

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
500 505 510

His Tyr Pro Val Glu Val Met Leu Lys  
515 520

<210> 72

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 72

atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacaggtgt ccactccca 60

gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 120

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180

ggaaagggcc tcgagtgggt cgagagagatt ttacctggaa gtaataattc tagataacaat 240

gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg 300

gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360

tttgcctggg ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc 420

aagggccat	cggcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccc	tggct	gcctggtaa	ggactacttc	cccgaaccgg	tgacggtgtc	540
ggcgc	ccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	600
tcc	ctcagca	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	660
aac	gtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	720
gaca	aaaactc	acacatgctg	tgtggagtgc	ccaccgtgcc	cagcac	780
aagat	cgcag	cctcaacat	ccagacattt	ggggagacca	agatgtccaa	840
gtcag	ctaca	ttgtgcagat	cctgagccgc	tacgacatcg	ccctggtcca	900
gacag	ccacc	tgactgccgt	ggggaaagctg	ctggacaacc	tcaatcagga	960
acctat	act	acgtggtcag	tgagccactg	ggacggaaca	gctataagga	1020
ttcgt	gtaca	ggcctgacca	ggtgtctgcg	gtggacagct	actactacga	1080
gagcc	ctgcg	ggaacgacac	cttcaaccga	gagccagcca	ttgtcagg	1140
ttcac	agagg	tcagggagtt	tgccattgtt	cccc	tgatggctgc	1200
gcc	gagat	cg	tgacgtctac	ctggatgtcc	aagagaaatg	1260
gac	gtcatgt	tgtggcga	cttcaatgcg	ggctgcagct	atgtgagacc	1320
tcatccat	cc	gcctgtggac	aagccccacc	ttccagtggc	tgatccccga	1380
acc	acagcta	cacccacgca	ctgtgcctat	gacaggatcg	tggttcagg	1440
cgaggg	ggcc	ttgttcccga	ctcggtctt	cccttaact	tccaggctgc	1500
agt	gaccaac	tggcccaagc	catcagtgc	cactatccag	tggaggtgat	1560

&lt;210&gt; 73

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 73	atgggatgga	gctgttatcat	ccttttttg	gtagcaacag	ctacaggtgt	ccactcc	60
	gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctc	agt	120

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaaggg actctggtca cagtctcctc agcctccacc	420
aaggcccatt cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacacccctc cccgctgtcc tacagtccctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgctg tgcgagttt ccaccgtgtc cagcaccaga gggcgggctg	780
aagatcgcag cttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc	840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900
gacagccacc tgactgccgt gggaaagctg ctggacaacc tcaatcagga cgcaccagac	960
acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgctacctg	1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tgatggctgc	1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccg	1140
ttcacagagg tcagggagtt tgccattgtt cccctgcattt cggccccggg ggacgcagta	1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttggag	1260
gacgtcatgt tgatggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac	1380
accacagcta cacccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc	1440
cgagggggccg ttgttcccgaa ctggctctt cccttaact tccaggctgc ctatggcctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga	1560

&lt;210&gt; 74

&lt;211&gt; 1569

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 74	
gccgccacca tggatggag ctgtatcatc ctttttgg tagaacacgc tacagggtgc	60
cactcccagg tgcaagctggt gcagtctgg gcagaggtga aaaagcctgg ggcctcagtg	120
aagggttcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaagggcct cgagtgggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggtcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg	540
tggaaactcag gcgccctgac cagcggcgtg cacaccccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctccca gcagcttggg caccctgacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg aaaaaactca cacatgtgt gtcgagtgac caccgtgtcc agcaccagag	780
ggcgggctga agatcgacgc cttcaacatc cagacatttgg gggagaccaa gatgtccaaat	840
gccaccctcg tcaagctacat tgtgcagatc ctgagccgct acgacatcgc cctggtccag	900
gaggtcagag acagccacct gactgccgtg gggaaagctgc tggacaacct caatcaggac	960
gcaccagaca cctatcacta cgtggtcagt gagccactgg gacggAACAG ctataaggag	1020
cgctacctgt tcgtgtacag gcctgaccag gtgtctggg tggacagcta ctactacgt	1080
gatggctgcg agccctgcgg gaacgacacc ttcaaccggag agccagccat tgtcaggttc	1140
ttctcccggt tcacagaggt cagggagttt gccattgttc ccctgcattgc ggccccgggg	1200
gacgcagtag ccgagatcga cgctcttat gacgtctacc tggatgtcca agagaaatgg	1260
ggcttggagg acgtcatgtt gatgggcac ttcaatgcgg gctgcagcta tgtgagaccc	1320
tcccagtgg catccatccg cctgtggaca agccccaccc tccagtggt gatccccgac	1380
agcgctgaca ccacagctac acccacgcac tgtgcctatg acaggatcgt ggtgcaggg	1440
atgctgctcc gagggggccgt tggccgcac tcggcttcc ccttaactt ccaggctgcc	1500
tatggcctga gtgaccaact ggcccaagcc atcagtgacc actatccagt ggaggtgatg	1560
ctgaagtga	1569

<210> 75  
<211> 1560  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 Fd - DNase I fusion  
<220>  
<221> CDS  
<222> (1)..(1560)  
<223>

<400> 75		
atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt		48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly		
1 5 10 15		
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag		96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys		
20 25 30		
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc		144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
35 40 45		
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc		192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu		
50 55 60		
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat		240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn		
65 70 75 80		
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac		288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn		
85 90 95		
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc		336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val		
100 105 110		
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc		384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly		
115 120 125		
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg		432

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser		
130						135						140					
gtc	ttc	ccc	ctg	gca	ccc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg		480	
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala		
145						150				155				160			
gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg		528
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val		
						165			170				175				
tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct		576
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala		
						180			185			190					
gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg		624
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val		
						195			200			205					
ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac		672
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His		
						210			215			220					
aag	ccc	agc	aac	acc	aag	gtg	gac	aag	aaa	gtt	gag	ccc	aaa	tct	tgt		720
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys		
						225			230			235			240		
gac	aaa	act	cac	aca	tgc	tgt	gtg	gag	tgc	cca	ccg	tgc	cca	gca	cct		768
Asp	Lys	Thr	His	Thr	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro		
						245			250			255					
gaa	ggc	ggg	ctg	aag	atc	gca	gcc	ttc	aac	atc	cag	aca	ttt	ggg	gag		816
Glu	Gly	Gly	Leu	Lys	Ile	Ala	Ala	Phe	Asn	Ile	Gln	Thr	Phe	Gly	Glu		
						260			265			270					
acc	aag	atg	tcc	aat	gcc	acc	ctc	gtc	agc	tac	att	gtg	cag	atc	ctg		864
Thr	Lys	Met	Ser	Asn	Ala	Thr	Leu	Val	Ser	Tyr	Ile	Val	Gln	Ile	Leu		
						275			280			285					
agc	cgc	tac	gac	atc	gcc	ctg	gtc	cag	gag	gtc	aga	gac	agc	cac	ctg		912
Ser	Arg	Tyr	Asp	Ile	Ala	Leu	Val	Gln	Glu	Val	Arg	Asp	Ser	His	Leu		
						290			295			300					
act	gcc	gtg	ggg	aag	ctg	ctg	gac	aac	ctc	aat	cag	gac	gca	cca	gac		960
Thr	Ala	Val	Gly	Lys	Leu	Leu	Asp	Asn	Leu	Asn	Gln	Asp	Ala	Pro	Asp		
						305			310			315			320		
acc	tat	cac	tac	gtg	gtc	agt	gag	cca	ctg	gga	cg	aac	agc	tat	aag		1008
Thr	Tyr	His	Tyr	Val	Val	Ser	Glu	Pro	Leu	Gly	Arg	Asn	Ser	Tyr	Lys		
						325			330			335					
gag	cgc	tac	ctg	ttc	gtg	tac	agg	cct	gac	cag	gtg	tct	gcg	gtg	gac		1056
Glu	Arg	Tyr	Leu	Phe	Val	Tyr	Arg	Pro	Asp	Gln	Val	Ser	Ala	Val	Asp		
						340			345			350					
agc	tac	tac	tac	gat	gat	ggc	tgc	gag	ccc	tgc	ggg	aac	gac	acc	ttc		1104
Ser	Tyr	Tyr	Tyr	Asp	Asp	Gly	Cys	Glu	Pro	Cys	Gly	Asn	Asp	Thr	Phe		
						355			360			365					

aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val 370 375 380	1152
agg gag ttt gcc att gtt ccc ctg cat gc <sup>g</sup> gcc ccg ggg gac gca gta Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val 385 390 395 400	1200
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys 405 410 415	1248
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gc <sup>g</sup> ggc tgc Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys 420 425 430	1296
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser 435 440 445	1344
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr 450 455 460	1392
ccc acg cac tgt gc <sup>c</sup> tat gac agg atc gtg gtt gca ggg atg ctg ctc Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu 465 470 475 480	1440
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala 485 490 495	1488
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr 500 505 510	1536
cca gtg gag gtg atg ctg aag tga Pro Val Glu Val Met Leu Lys 515	1560

&lt;210&gt; 76

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 76

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15
--

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro

245

250

255

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
500 505 510

Pro Val Glu Val Met Leu Lys  
515

<210> 77

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 77  
atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacagggtgt ccactcccaag  
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 60  
tgcaaggcctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca  
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa gtaataattc tagatacaat 120  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg  
gagctcagca gcctgagggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 180  
tttgcctggc ttgcttactg gggccaaggg actctggtca cagtcctc caccctccacc  
aaggcccattt cggctttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg 240  
gcacctgggt gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca  
ggcgcctga ccagcggcgt gcacaccttc ccggctgtcc tacagtccctc aggactctac 300  
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc  
aacgtgaatc acaagccccag caacaccaag gtggacaaga aagttgagcc caaatcttgt 360  
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcaggctg  
aagatcgcag ccttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc 420  
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga  
gacagccacc tgactgccgt ggagaagctg ctggacaacc tcaatcagga cgcaccagac 480  
900  
960

acctatcact acgtggtcag tgagccactg ggacggaaca gctataagga gcgctacctg	1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tcatggctgc	1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctcccg	1140
ttcacagagg tcagggagtt tgccattgtt cccctgcatt cggccccggg ggacgcagta	1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgag	1260
gacgtcatgt tcatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtgcc tcatccccga cagcgctgac	1380
accacagcta cacccacgca ctgtgcctat gacaggatcg tgggtgcagg gatgctgctc	1440
cgagggggccg ttgttcccga ctggctctt cccttaact tccaggctgc ctatggcctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga	1560

&lt;210&gt; 78

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 78	
atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacaggtgt ccactccag	60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataaat	240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtcaag atcctacgac	360
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc	420
aaggggccat cggcttccc cctggcaccc tcctccaaga gcacccctgg gggcacagcg	480
gccctggct gcctggtaa ggactacttc cccgaaccgg tgacggtgcc gtggaaactca	540
ggcgccctga ccagcggcgt gcacaccccttc cccggctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720

gacaaaactc acacatgctg tgtcgagtgt ccaccgtgtc cagcaccaga gggcaggctg	780
aagatcgca cttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc	840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900
gacagccacc tgactgccgt ggagaagctg ctggacaacc tcaatcagga cgccaccagac	960
acctatactact acgtggtcag tgagccactg ggacggaaca gctataagga gcgcatactg	1020
ttcgtgtaca ggcctgacca ggtgtctgcg gtggacagct actactacga tcatggctgc	1080
gagccctgcg ggaacgacac cttcaaccga gagccagcca ttgtcagggtt cttctccgg	1140
ttcacagagg tcagggagtt tgccattgtt cccctgcattt cggccccggg ggacgcagta	1200
gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttgag	1260
gacgtcatgt tcatgggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tcatccccga cagcgctgac	1380
accacagcta cacccacgca ctgtgcctat gacaggatcg tggttgcagg gatgctgctc	1440
cgagggggccg ttgttcccga ctggctctt cccttaact tccaggctgc ctatggctg	1500
agtgaccaac tggcccaagc catcagtgac cactatccag tggaggtgat gctgaagtga	1560

<210> 79

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<220>

<221> CDS

<222> (1)..(1560)

<223>

<400> 79

atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt	48
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1 5 10 15	

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu 50 55 60	192
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn 65 70 75 80	240
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95	288
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125	384
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140	432
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175	528
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190	576
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205	624
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220	672
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240	720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245 250 255	768

gaa ggc agg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu 260 265 270	816
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu 275 280 285	864
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu 290 295 300	912
act gcc gtg gag aag ctg ctg gac aac ctc aat cag gac gca cca gac Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp 305 310 315 320	960
acc tat cac tac gtg gtc agt gag cca ctg gga cgga aac agc tat aag Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys 325 330 335	1008
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp 340 345 350	1056
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe 355 360 365	1104
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val 370 375 380	1152
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val 385 390 395 400	1200
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys 405 410 415	1248
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys 420 425 430	1296
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser 435 440 445	1344
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr 450 455 460	1392
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu 465 470 475 480	1440
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala	1488

485                    490                    495

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gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat      1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr
      500          505          510

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cca gtg gag gtg atg ctg aag tga 1560  
Pro Val Glu Val Met Leu Lys  
515

<210> 80

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 80

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
           100                 105                 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Arg Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Glu Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala  
 485 490 495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
 500 505 510

Pro Val Glu Val Met Leu Lys  
 515

<210> 81

<211> 1578

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 81  
 atgggatgga gctgttatcat cctcttcttg gtagcaacag ctacagggtgt ccactccag 60  
 gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc 120

tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cgagagatt ttacctggaa gtaataattc tagataacaat	240
gagaagttca aggcccgagt gacagtcaact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360
tttgcctgggt ttgcttactg gggccaagg actctggtca cagtcctc agcctccacc	420
aagggcccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540
ggcgccctga ccagcggcgt gcacacccctc cccgctgtcc tacagtcctc aggactctac	600
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcacccagac ctacatctgc	660
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgccc accgtgccc gcacacctgaag gcgggctgaa gatcgagcc	780
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840
gtcagatcc tgagccgcta cgacatcgcc ctggccagg aggtcagaga cagccacctg	900
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020
cctgaccagg tgtctcggt ggacagctac tactacgatg atggctgcga gccctgcggg	1080
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc	1140
agggagtttgc ccattgttcc cctgcatgctg gccccgggg acgcagtagc cgagatcgac	1200
gctctctatg acgtctaccc ggtatgtccaa gagaaatggg gcttggagga cgtcatgttgc	1260
atgggcgact tcaatgcggg ctgcagctat gtgagacccct cccagtggtc atccatccgc	1320
ctgtggacaa gccccaccc ttccagtgatgctg atccccgaca gcgctgacac cacagctaca	1380
cccacgcact gtgcctatga caggatcgatg gttgcagggta tgctgctccg agggggccgtt	1440
gttcccgact cggctttcc cttaacttc caggctgcct atggcctgag tgaccaactg	1500
gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagggggg cggacccaaa	1560
aagaagcgca agtttga	1578

&lt;210&gt; 82

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 82		
atgggatgga gctgttatcat cctttcttg gtagcaacag ctacaggtgt ccactccag	60	
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc	120	
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180	
ggaaagggcc tcgagtggtt cgagagatt ttacctggaa gtaataattc tagataacaat	240	
gagaagttca agggccgagt gacagtca act agagacacat ccacaaacac agcctacatg	300	
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360	
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtcctc agcctccacc	420	
aagggccat cggcttccc cctggcaccc tcctccaaga gcacctctgg gggcacagcg	480	
gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacgggtgc gtggactca	540	
ggcgccctga ccagcggcgt gcacaccttc cccgctgtcc tacagtccctc aggactctac	600	
tccctcagca gcgtggtgac cgtccctcc agcagcttgg gcacccagac ctacatctgc	660	
aacgtgaatc acaagcccag caacaccaag gtggacaaga aagttgagcc caaatcttgt	720	
gacaaaactc acacatgtcc accgtgtcca gcaccagagg gcgggctgaa gatgcagcc	780	
ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt	840	
gtcagatcc tgagccgcta cgacatcgcc ctggtccagg aggtcagaga cagccacctg	900	
actgccgtgg ggaagctgct ggacaacctc aatcaggacg caccagacac ctatcactac	960	
gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg	1020	
cctgaccagg tgtctgcggt ggacagctac tactacgtat atggctgcga gccctgcggg	1080	
aacgacacct tcaaccgaga gccagccatt gtcaggttct tctccgggtt cacagaggtc	1140	
agggagttt ccattgttcc cctgcatgcg gccccgggg acgcagtagc cgagatcgac	1200	
gctctctatg acgtctaccc ggtatgtccaa gagaaatggg gcttggagga cgtcatgtt	1260	
atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggc atccatccgc	1320	
ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca	1380	
cccacgcact gtgcctatga caggatcgatg gttgcaggga tgctgctccg agggccggtt	1440	
gttcccgact cggtcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg	1500	

gccccaaagcca tcagtgcacca ctatccagtg gaggtgatgc tgaagggggg cggaacccaaa	1560
aagaagcgca aggttga	1578

<210> 83

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 83	
gccggccacca tggatggag ctgtatcatc ctcttcttgg tagcaacagc tacaggtgtc	60
cactcccagg tgcaagctgg gcagtctgg gcagaggtaaaaaggctgg ggcctcagtg	120
aagggtgtcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaaggccct cgagtgggtc ggagagattt tacctggaag taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctgggt tgcttactgg ggccaaggga ctctggtcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggctg cctggtaag gactacttcc ccgaaccgggt gacgggtgtcg	540
tggaaactcag gcgcctgac cagcggcgtg cacaccccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgcctcca gcagcttggg cacccagacc	660
tacatctgca acgtaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaactca cacatgtcca cogtgtccag caccagaggg cgggctgaag	780
atcgccagcct tcaacatcca gacatttggg gagaccaaga tgtccaatgc caccctcgcc	840
agctacattg tgcagatcct gagccgctac gacatcgccc tggccagga ggtcagagac	900
agccacctga ctgccgtggg gaagctgctg gacaacctca atcaggacgc accagacacc	960
tatcactacg tggtcagtga gccactggga cggAACAGCT ataaggagcg ctacctgttc	1020
gtgtacaggc ctgaccagggt gtctgcggtg gacagctact actacgatga tggctgcgag	1080
ccctgcggga acgacacctt caaccgagag ccagccattt tcaggttctt ctcccggttc	1140
acagaggtaa gggagttgc cattgttccc ctgcattgcgg cccgggggaa cgcagtagcc	1200

gagatcgacg ctcttatga cgtctacctg gatgtccaag agaaatgggg cttggaggac 1260  
 gtcatgttga tggcgactt caatgcggc tgcagctatg tgagaccctc ccagtggta 1320  
 tccatccgcc tgtggacaag ccccaccttc cagtggtga tccccgacag cgctgacacc 1380  
 acagctacac ccacgcactg tgcctatgac aggatcgtgg ttgcagggat gctgctccga 1440  
 ggggcccgttgc ttcccgaactc ggctcttccc tttaacttcc aggctgccta tggcctgagt 1500  
 gaccaactgg cccaaagccat cagtgaccac tatccagtg aggtgatgct gaagggggc 1560  
 ggacccaaaa agaagcgcaa ggtttga 1587

&lt;210&gt; 84

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1578)

&lt;223&gt;

<400> 84  
 atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct aca ggt 48  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 1 5 10 15

gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192  
 Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240  
 Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn

65	70	75	80	
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn 85 90 95 288				
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110 336				
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly 115 120 125 384				
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130 135 140 432				
gtc ttc ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145 150 155 160 480				
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165 170 175 528				
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180 185 190 576				
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195 200 205 624				
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210 215 220 672				
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225 230 235 240 720				
gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa ggc ggg ctg Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Leu 245 250 255 768				
aag atc gca gcc ttc aac atc cag aca ttt ggg gag acc aag atg tcc Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser 260 265 270 816				
aat gcc acc ctc gtc agc tac att gtg cag atc ctg agc cgc tac gac Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp 275 280 285 864				
atc gcc ctg gtc cag gag gtc aga gac agc cac ctg act gcc gtg ggg Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly 290 295 300 912				
aag ctg ctg gac aac ctc aat cag gac gca cca gac acc tat cac tac 960				

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr			
305	310	315	320
gtg gtc agt gag cca ctg gga cg aac agc tat aag gag cgc tac ctg			1008
Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu			
325	330	335	
ttc gtg tac agg cct gac cag gtg tct gcg gtg gac agc tac tac tac			1056
Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr			
340	345	350	
gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc aac cga gag cca			1104
Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro			
355	360	365	
gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc agg gag ttt gcc			1152
Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala			
, 370	375	380	
att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta gcc gag atc gac			1200
Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp			
385	390	395	400
gct ctc tat gac gtc tac ctg gat gtc caa gag aaa tgg ggc ttg gag			1248
Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu			
405	410	415	
gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc agc tat gtg aga			1296
Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg			
420	425	430	
ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc ccc acc ttc cag			1344
Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln			
435	440	445	
tgg ctg atc ccc gac agc gct gac acc aca gct aca ccc acg cac tgt			1392
Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys			
450	455	460	
gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc cga ggg gcc gtt			1440
Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val			
465	470	475	480
gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct gcc tat ggc ctg			1488
Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu			
485	490	495	
agt gac caa ctg gcc caa gcc atc agt gac cac tat cca gtg gag gtg			1536
Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val			
500	505	510	
atg ctg aag ggg ggc gga ccc aaa aag aag cgc aag gtt tga			1578
Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys Val			
515	520	525	

<211> 525

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 85

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
						20		25					30		

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
					35		40					45			

Ser	Ala	Tyr	Trp	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					50		55		60						

Glu	Trp	Val	Gly	Glu	Ile	Leu	Pro	Gly	Ser	Asn	Asn	Ser	Arg	Tyr	Asn
				65		70			75				80		

Glu	Lys	Phe	Lys	Gly	Arg	Val	Thr	Val	Thr	Arg	Asp	Thr	Ser	Thr	Asn
					85			90				95			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
					100			105				110			

Tyr	Tyr	Cys	Ala	Arg	Ser	Tyr	Asp	Phe	Ala	Trp	Phe	Ala	Tyr	Trp	Gly
					115			120			125				

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
					130		135				140				

Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
					145		150			155			160		

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
					165			170				175			

Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180

185

190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Gly Gly Leu  
 245 250 255

Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys Met Ser  
 260 265 270

Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp  
 275 280 285

Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly  
 290 295 300

Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr  
 305 310 315 320

Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu  
 325 330 335

Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp Ser Tyr Tyr Tyr  
 340 345 350

Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe Asn Arg Glu Pro  
 355 360 365

Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val Arg Glu Phe Ala  
 370 375 380

Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile Asp  
 385 390 395 400

Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu  
 405 410 415

Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg  
 420 425 430

Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln  
 435 440 445

Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr Pro Thr His Cys  
 450 455 460

Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu Arg Gly Ala Val  
 465 470 475 480

Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala Ala Tyr Gly Leu  
 485 490 495

Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val Glu Val  
 500 505 510

Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys Val  
 515 520 525

<210> 86

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 86		
atgggatgga gctgttatcat ccttttcttg gtagcaacag ctacaggtgt ccactcccag		60
gtgcagctgg tgcagtctgg ggcagaggtg aaaaagcctg gggcctcagt gaaggtgtcc		120
tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca		180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat		240
gagaagttca agggccgagt gacagtcaact agagacacat ccacaaacac agcctacatg		300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac		360
tttgccttgtt ttgcttactg gggccaagg actctggtca cagtctcctc agcctccacc		420
aagggccat cggtcttccc cctggcaccc tcctccaaga gcacccctgg gggcacagcg		480

gccctgggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtgtc	gtggaaactca	540
ggcgccctga	ccagcggcgt	gcacaccccttc	ccggctgtcc	tacagtcctc	aggactctac	600
tccctcagca	gcgtggtgac	cgtgccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
gacaaaactc	acacatgctg	tgtggagtgc	ccaccgtgcc	cagcacctga	agggagcggc	780
gggctgaaga	tcgcagcatt	caacatccag	acatttgggg	agaccaagat	gtccaatgcc	840
accctcgta	gctacattgt	gcagatcctg	agccgctacg	acatcgccct	ggtccaggag	900
gtcagagaca	gccacctgac	tgccgtgggg	aagctgctgg	acaaccta	tcaggacgca	960
ccagacacct	atcaactacgt	ggtcagttag	ccactggac	ggaacagcta	taaggagcgc	1020
tacctgttcg	tgtacaggcc	tgaccaggtg	tctgcggtgg	acagctacta	ctacgatgat	1080
ggctgcgagc	cctgcgggaa	cgacacccctc	aaccgagac	cagccattgt	caggttcttc	1140
tcccggttca	cagaggtcag	ggagttgcc	attgttcccc	tgcatgcggc	cccgaaaaac	1200
gcagtagccg	agatcgacgc	tctctatgac	gtctacctgg	atgtccaaga	gaaatggggc	1260
ttggaggacg	tcatgttgat	gggcgacttc	aatgcgggct	gcagctatgt	gagaccctcc	1320
cagtggtcat	ccatccgcct	gtggacaaggc	cccacccctcc	agtggctgat	ccccgacacgc	1380
gctgacacca	cagctacacc	cacgcactgt	gcctatgaca	ggatcgtgg	tgcaggatg	1440
ctgctccgag	ggccggttgt	tcccgactcg	gctctccct	ttaacttcca	ggctgcctat	1500
ggcctgagtg	accaactggc	ccaagccatc	agtgaccact	atccagtgg	ggtgatgctg	1560
aaggggggcg	gacccaaaaa	gaagcgcaag	gtttga			1596

<210> 87

<211> 1596

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 87	atgggatgga	gctgttatcat	cctcttcttg	gtagcaacag	ctacaggtgt	ccactcccag	60
	gtgcagctgg	tgcagtctgg	ggcagaggtg	aaaaagcctg	gggcctcagt	gaaggtgtcc	120
	tgcaaggctt	ctggctacac	cttcagtgcc	tactggatag	agtgggtgcg	ccaggctcca	180

ggaaagggcc	tcgagtgggt	cggagagatt	ttacctggaa	gtaataattc	tagataacaat	240
gagaagttca	aggcccgagt	gacagtcaact	agagacacat	ccacaaacac	agcctacatg	300
gagctcagca	gcctgaggc	tgaggacaca	gccgtctatt	actgtgcaag	atcctacgac	360
tttgccttgtt	ttgcttactg	gggccaaggg	actctggtca	cagtctcctc	agcctccacc	420
aagggccat	cggcttccc	cctggcaccc	tcctccaaga	gcacctctgg	gggcacagcg	480
gccctggct	gcctggtcaa	ggactacttc	cccgaaccgg	tgacggtg	gtggactca	540
ggcgccctga	ccagcggcgt	gcacaccc	ccggctgtcc	tacagtcc	aggactctac	600
tccctcagca	gcgtggtgac	cgtccctcc	agcagcttgg	gcacccagac	ctacatctgc	660
aacgtgaatc	acaagcccag	caacaccaag	gtggacaaga	aagttgagcc	caaatcttgt	720
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gtcagagaca	gccacctgac	tgccgtgggg	aagctgctgg	acaaccta	tcaggacgca	960
ccagacacct	atcactacgt	ggtcagtgag	ccactgggac	ggaacagcta	taaggagcgc	1020
tacctgttgc	tgtacaggcc	tgaccagg	tctgcgtgg	acagctacta	ctacgatgat	1080
ggctgcgagc	cctgcgggaa	cgacaccc	aaccgagagc	cagccattgt	caggttctc	1140
tccccgttca	cagaggtcag	ggagtttgc	attgttccc	tgcatgcggc	cccgggggac	1200
gcagtagccg	agatcgacgc	tctctatgac	gtctacctgg	atgtccaaga	gaaatggggc	1260
ttggaggacg	tcatgttgc	gggcgacttc	aatgcgggct	gcagctatgt	gagaccctcc	1320
cagtggtcat	ccatccgcct	gtggacaagc	cccaccc	agtggctgat	ccccgacagc	1380
gctgacacca	cagctacacc	cacgcactgt	gcctatgaca	ggatcgtgg	tgcagggatg	1440
ctgctccgag	ggccgttgt	tcccgactcg	gctctccct	ttaacttcca	ggctgcctat	1500
ggcctgagtg	accaactggc	ccaagccatc	agtgaccact	atccagtgg	ggtgatgctg	1560
aaggggggcg	gacccaaaaa	gaagcgcaag	gtttga			1596

&lt;210&gt; 88

&lt;211&gt; 1605

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

<400> 88	
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aagggtgcct gcaaggcttc tggctacacc ttcaagtgcct actggataga gtgggtgcgc	180
caggctccag gaaagggcct cgagtgggtc ggagagattt taccttggaa taataattct	240
agataacaatg agaagttcaa gggccgagtg acagtcacta gagacacatc cacaacacaca	300
gcctacatgg agctcagcag cctgaggtct gaggacacag ccgtcttatta ctgtgcaaga	360
tcctacgact ttgcctggtt tgcttactgg ggccaaggga ctctggtcac agtctcctca	420
gcctccacca agggccatc ggtttcccc ctggcacccct cctccaagag cacctctggg	480
ggcacagcgg ccctgggtcg cctggtaag gactacttcc ccgaaccggg gacgggtcg	540
tggaaactcag gcccctgac cagcggcggt cacaccccttcc cggctgtcct acagtcctca	600
ggactctact ccctcagcag cgtggtgacc gtgccttcca gcagcttggg cacccagacc	660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc	720
aaatcttgtg acaaaactca cacatgtgt gtcgagtgtc caccgtgtcc agcaccagag	780
gggagcggcg ggctgaagat cgccgccttc aacatccaga catttgggg gaccaagatg	840
tccaatgcca ccctcgtag ctacattgtg cagatcctga gccgctacga catcgccctg	900
gtccaggagg tcagagacag ccacctgact gccgtgggg agctgcttggca aacactcaat	960
caggacgcac cagacaccta tcactacgtg gtcagtgtc cactggacg gaacagctat	1020
aaggagcgct acctgttcgt gtacaggcct gaccaggtgt ctgcgggtgg cagctactac	1080
tacgatgatg gctgcgagcc ctgcgggaac gacacccatca accgagagcc agccattgtc	1140
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gcagggatgc tgctccgagg ggccgtgtt cccgactcgg ctcttccctt taacttccag	1500
gctgcctatg gcctgagtga ccaactggcc caagccatca gtgaccacta tccagtggag	1560

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 <211> 1596  
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 <223> Humanised HMFG1 Fd - DNase I fusion  
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 <221> CDS  
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 1 5 10 15  
 gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag 96  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30  
 cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc 144  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45  
 agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc 192  
 Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60  
 gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat 240  
 Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80  
 gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac 288  
 Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95  
 aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110  
 tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc 384  
 Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser 130	135	140	432	
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala 145	150	155	160	480
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val 165	170	175	528	
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala 180	185	190	576	
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val 195	200	205	624	
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His 210	215	220	672	
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys 225	230	235	240	720
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro 245	250	255	768	
gaa ggg agc ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe 260	265	270	816	
ggg gag acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln 275	280	285	864	
atc ctg agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser 290	295	300	912	
cac ctg act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala 305	310	315	960	
cca gac acc tat cac tac gtg gtc agt gag cca ctg gga cg <sup>g</sup> aac agc Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser 325	330	335	1008	
tat aag gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala 340	345	350	1056	
gtg gac agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp			1104	

355	360	365	
acc ttc aac cga gag cca gcc att gtc agg ttc ttc tcc cg <sup>g</sup> ttc aca Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr 370	375	380	1152
gag gtc agg gag ttt gcc att gtt ccc ctg cat gc <sup>g</sup> gcc ccg ggg gac Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp 385	390	395	1200
gca gta gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln 405	410	415	1248
gag aaa tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gc <sup>g</sup> Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala 420	425	430	1296
ggc tgc agc tat gtg aga ccc tcc cag tgg tca tcc atc cg <sup>c</sup> ctg tgg Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp 435	440	445	1344
aca agc ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr 450	455	460	1392
gct aca ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met 465	470	475	1440
ctg ctc cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe 485	490	495	1488
cag gct gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp 500	505	510	1536
cac tat cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys 515	520	525	1584
cg <sup>c</sup> aag gtt tga Arg Lys Val 530			1596
<210> 90			
<211> 531			
<212> PRT			
<213> Artificial Sequence			
<220>			

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 90

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225                    230                    235                    240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245                    250                    255

Glu Gly Ser Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe  
 260                    265                    270

Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln  
 275                    280                    285

Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser  
 290                    295                    300

His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala  
 305                    310                    315                    320

Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser  
 325                    330                    335

Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala  
 340                    345                    350

Val Asp Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp  
 355                    360                    365

Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr  
 370                    375                    380

Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp  
 385                    390                    395                    400

Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln  
 405                    410                    415

Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala  
 420                    425                    430

Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp  
 435                    440                    445

Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr  
 450                    455                    460

Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met  
465 470 475 480

Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe  
485 490 495

Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp  
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His Tyr Pro Val Glu Val Met Leu Lys Gly Gly Gly Pro Lys Lys Lys  
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Arg Lys Val  
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<210> 91

<211> 1590

<212> DNA

<220>

<400> 91  
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca 180  
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagataacaat 240  
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg 300  
gagctcagca gcctgaggtc tgaggacaca gccgtctatt actgtgcaag atcctacgac 360  
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gccctggct gcctggtcaa ggactacttc cccgaaccgg tgacggtgac gtggaaactca 540  
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aacgtgaatc acaagccccag caacacccaag gtggacaaga aagttgagcc caaatcttgt	720
gacaaaactc acacatgctg tgtggagtgc ccaccgtgcc cagcacctga aggcgggctg	780
aagatcgca gcttcaacat ccagacattt ggggagacca agatgtccaa tgccaccctc	840
gtcagctaca ttgtgcagat cctgagccgc tacgacatcg ccctggtcca ggaggtcaga	900
gacagccacc tgactgccgt ggggaagctg ctggacaacc tcaatcagga cgccaccagac	960
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gccgagatcg acgctctcta tgacgtctac ctggatgtcc aagagaaatg gggcttggag	1260
gacgtcatgt tgatggcga cttcaatgcg ggctgcagct atgtgagacc ctcccagtgg	1320
tcatccatcc gcctgtggac aagccccacc ttccagtggc tgatccccga cagcgctgac	1380
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cgagggggccg ttgttcccga ctcggctctt ccctttaact tccaggctgc ctatggcctg	1500
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<210> 92

<211> 1590

<212> DNA

<213> Artificial Sequence

<220>

<223> Humanised HMFG1 Fd - DNase I fusion

<400> 92	
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tgcaaggctt ctggctacac cttcagtgcc tactggatag agtgggtgcg ccaggctcca	180
ggaaagggcc tcgagtgggt cggagagatt ttacctggaa gtaataattc tagatacaat	240
gagaagttca agggccgagt gacagtcact agagacacat ccacaaacac agcctacatg	300
gagctcagca gcctgaggc tgaggacaca gccgtctatt actgtgcaag atcctacgac	360

tttgcctgg	ttgttactg	ggccaagg	actctgg	tca	cagtctcc	tc	agcctccacc	420									
aaggccc	at	cggtttccc	cctggcaccc	tcctccaaga	gcac	ctctgg	ggcacagcg	480									
gc	cc	ctgg	gtcaa	ggactacttc	cccgaaccgg	tgacgg	gtc	gtggaa	ctca	540							
ggc	gc	cc	ctgtcaa	ggactacttc	cccgaaccgg	tgacgg	gtc	gtggaa	ctca	600							
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gcc	gag	atcg	ac	g	ct	ct	ct	tc	gg	gtc	act	atcg	cc	cc	at	gg	1260
gac	gt	cat	gt	gg	tc	at	tc	at	gg	gtc	act	atcg	cc	cc	at	gg	1320
tca	tc	ccat	cc	tc	gt	tc	at	tc	gg	gtc	act	atcg	cc	cc	at	gg	1380
acc	ac	ag	cc	ac	gc	tc	tt	cc	at	gt	gt	atcg	cc	cc	at	gg	1440
cg	aggg	gg	cc	cc	cc	cc	tt	cc	tt	cc	at	cc	cc	at	gg	cc	1500
agt	gac	ca	ac	tgg	cc	aa	gc	ca	t	c	at	cc	cc	at	gg	gt	1560
ggc	gg	ac	cc	aa	gg	aa	gg	cc	tt	cc	at	gg	cc	at	gg	tt	1590

&lt;210&gt; 93

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;400&gt; 93

gccgccacca tggatggag ctgtatcatc ctcttcttgg tagcaacagc tacagggtgc	60
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cgctacctgt tcgtgtacag gcctgaccag gtgtctgcgg tggacagcta ctactacgt	1080
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ttctcccggt tcacagaggt cagggagttt gccattgttc ccctgcatgc ggccccgggg	1200
gacgcagtag ccgagatcga cgctcttat gacgtctacc tggatgtcca agagaaatgg	1260
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tatggcctga gtgaccaact ggcccaagcc atcagtgacc actatccagt ggaggtgatg	1560
ctgaaggggg gcggacccaa aaagaagcgc aaggttga	1599

&lt;210&gt; 94

&lt;211&gt; 1590

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Humanised HMFG1 Fd - DNase I fusion

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1590)

&lt;223&gt;

<400>	94		
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1 5 10 15			
gtc cac tcc cag gtg cag ctg gtg cag tct ggg gca gag gtg aaa aag			96
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys			
20 25 30			
cct ggg gcc tca gtg aag gtg tcc tgc aag gct tct ggc tac acc ttc			144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe			
35 40 45			
agt gcc tac tgg ata gag tgg gtg cgc cag gct cca gga aag ggc ctc			192
Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
50 55 60			
gag tgg gtc gga gag att tta cct gga agt aat aat tct aga tac aat			240
Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn			
65 70 75 80			
gag aag ttc aag ggc cga gtg aca gtc act aga gac aca tcc aca aac			288
Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn			
85 90 95			
aca gcc tac atg gag ctc agc agc ctg agg tct gag gac aca gcc gtc			336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val			
100 105 110			
tat tac tgt gca aga tcc tac gac ttt gcc tgg ttt gct tac tgg ggc			384
Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly			
115 120 125			
caa ggg act ctg gtc aca gtc tcc tca gcc tcc acc aag ggc cca tcg			432
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser			
130 135 140			
gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg			480
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala			

145	150	155	160	
gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val				528
165                    170                    175				
tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala				576
180                    185                    190				
gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val				624
195                    200                    205				
ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His				672
210                    215                    220				
aag ccc agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt Lys Pro Ser Asn Thr Lys Val Asp Lys Val Glu Pro Lys Ser Cys				720
225                    230                    235                    240				
gac aaa act cac aca tgc tgt gtg gag tgc cca ccg tgc cca gca cct Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro				768
245                    250                    255				
gaa ggc ggg ctg aag atc gca gcc ttc aac atc cag aca ttt ggg gag Glu Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu				816
260                    265                    270				
acc aag atg tcc aat gcc acc ctc gtc agc tac att gtg cag atc ctg Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu				864
275                    280                    285				
agc cgc tac gac atc gcc ctg gtc cag gag gtc aga gac agc cac ctg Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu				912
290                    295                    300				
act gcc gtg ggg aag ctg ctg gac aac ctc aat cag gac gca cca gac Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp				960
305                    310                    315                    320				
acc tat cac tac gtg gtc agt gag cca ctg gga cgg aac agc tat aag Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys				1008
325                    330                    335				
gag cgc tac ctg ttc gtg tac agg cct gac cag gtg tct gcg gtg gac Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp				1056
340                    345                    350				
agc tac tac tac gat gat ggc tgc gag ccc tgc ggg aac gac acc ttc Ser Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe				1104
355                    360                    365				
aac cga gag cca gcc att gtc agg ttc ttc tcc cgg ttc aca gag gtc Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val				1152
370                    375                    380				
agg gag ttt gcc att gtt ccc ctg cat gcg gcc ccg ggg gac gca gta				1200

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val			
385	390	395	400
gcc gag atc gac gct ctc tat gac gtc tac ctg gat gtc caa gag aaa			1248
Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys			
405	410	415	
tgg ggc ttg gag gac gtc atg ttg atg ggc gac ttc aat gcg ggc tgc			1296
Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys			
420	425	430	
agc tat gtg aga ccc tcc cag tgg tca tcc atc cgc ctg tgg aca agc			1344
Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser			
435	440	445	
ccc acc ttc cag tgg ctg atc ccc gac agc gct gac acc aca gct aca			1392
Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr			
450	455	460	
ccc acg cac tgt gcc tat gac agg atc gtg gtt gca ggg atg ctg ctc			1440
Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu			
465	470	475	480
cga ggg gcc gtt gtt ccc gac tcg gct ctt ccc ttt aac ttc cag gct			1488
Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala			
485	490	495	
gcc tat ggc ctg agt gac caa ctg gcc caa gcc atc agt gac cac tat			1536
Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr			
500	505	510	
cca gtg gag gtg atg ctg aag ggg ggc gga ccc aaa aag aag cgc aag			1584
Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Lys Arg Lys			
515	520	525	
gtt tga			1590
Val			

<210> 95  
<211> 529  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Humanised HMFG1 Fd - DNase I fusion  
<400> 95

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
 35 40 45

Ser Ala Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

Glu Trp Val Gly Glu Ile Leu Pro Gly Ser Asn Asn Ser Arg Tyr Asn  
 65 70 75 80

Glu Lys Phe Lys Gly Arg Val Thr Val Thr Arg Asp Thr Ser Thr Asn  
 85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 100 105 110

Tyr Tyr Cys Ala Arg Ser Tyr Asp Phe Ala Trp Phe Ala Tyr Trp Gly  
 115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
 130 135 140

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
 145 150 155 160

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 165 170 175

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 180 185 190

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 195 200 205

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 210 215 220

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 225 230 235 240

Asp Lys Thr His Thr Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro  
 245 250 255

Glu Gly Gly Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu  
 260 265 270

Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu  
 275 280 285

Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp Ser His Leu  
 290 295 300

Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp Ala Pro Asp  
 305 310 315 320

Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn Ser Tyr Lys  
 325 330 335

Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser Ala Val Asp  
 340 345 350

Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn Asp Thr Phe  
 355 360 365

Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
 370 375 380

Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val  
 385 390 395 400

Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys  
 405 410 415

Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys  
 420 425 430

Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu Trp Thr Ser  
 435 440 445

Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr Thr Ala Thr  
 450 455 460

Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly Met Leu Leu  
 465 470 475 480

Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln Ala

485

490

495

Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr  
500 505 510

Pro Val Glu Val Met Leu Lys Gly Gly Pro Lys Lys Arg Lys  
515 520 525

Val

<210> 96

<211> 7

<212> PRT

<213> Simian virus 40

<400> 96

Pro Lys Lys Lys Arg Lys Val  
1 5

<210> 97

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide linker

<400> 97

Gly Ser Gly Gly  
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<210> 98

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus ribosome binding sequence

<400> 98  
gccggccacc

9

<210> 99

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein

<400> 99

Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro  
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Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp Thr Arg Pro Pro Asp  
20 25 30

Thr Arg Pro  
35

<210> 100

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant hinge

<400> 100

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Glu  
1 5 10

150

<210> 101

<211> 5

<212> PRT

*A<sup>35</sup>  
act*  
<213> Homo sapiens

<400> 101

Ala Pro Asp Thr Arg  
1                       5

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